

OM protein - protein search, using sw model

Run on: December 13, 2004, 18:48:47 ; Search time 116.022 Seconds  
(without alignments)  
426.682 Million cell updates/sec

Title: US-10-010-942B-4 ,  
Perfect score: 719  
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result<br>No. | Score | %<br>Query |        | DB | ID       | Description        |
|---------------|-------|------------|--------|----|----------|--------------------|
|               |       | Match      | Length |    |          |                    |
| 1             | 718   | 99.9       | 138    | 5  | ABG76924 | Abg76924 Mouse 3D6 |
| 2             | 652   | 90.7       | 138    | 5  | ABG76928 | Abg76928 Humanised |
| 3             | 651   | 90.5       | 468    | 6  | ABP58275 | Abp58275 Humanised |
| 4             | 650   | 90.4       | 138    | 5  | ABG76932 | Abg76932 Humanised |
| 5             | 609.5 | 84.8       | 133    | 6  | ABG74243 | Abg74243 Mouse ant |
| 6             | 578.5 | 80.5       | 139    | 6  | ABG74247 | Abg74247 Mouse ant |
| 7             | 578   | 80.4       | 462    | 6  | AAO29869 | Aao29869 Mouse ant |
| 8             | 578   | 80.4       | 462    | 7  | ADJ79787 | Adj79787 TRA-8 ant |
| 9             | 578   | 80.4       | 464    | 5  | AAU72801 | Aau72801 TRA-8 hea |

|    |       |      |     |   |          |          |           |
|----|-------|------|-----|---|----------|----------|-----------|
| 10 | 573   | 79.7 | 138 | 2 | AAR20064 | Aar20064 | MRK16-H c |
| 11 | 569   | 79.1 | 144 | 5 | ABB79730 | Abb79730 | Anti-Stre |
| 12 | 568   | 79.0 | 139 | 2 | AAR30480 | Aar30480 | hCEA spec |
| 13 | 566   | 78.7 | 140 | 5 | AAU76122 | Aau76122 | Mouse mon |
| 14 | 564   | 78.4 | 139 | 2 | AAR27053 | Aar27053 | Anti-CEA  |
| 15 | 564   | 78.4 | 140 | 5 | AAU76133 | Aau76133 | Mouse mAb |
| 16 | 563   | 78.3 | 138 | 2 | AAW03722 | Aaw03722 | Anti-huma |
| 17 | 561   | 78.0 | 140 | 5 | AAU76132 | Aau76132 | Mouse mAb |
| 18 | 560   | 77.9 | 138 | 3 | AAV32404 | Aay32404 | Mouse ant |
| 19 | 559   | 77.7 | 140 | 6 | ABG74241 | Abg74241 | Mouse ant |
| 20 | 557.5 | 77.5 | 137 | 2 | AAW57592 | Aaw57592 | Chimeric  |
| 21 | 557.5 | 77.5 | 137 | 2 | AAW89625 | Aaw89625 | Mouse hum |
| 22 | 557.5 | 77.5 | 137 | 3 | AAV77513 | Aay77513 | Mouse ant |
| 23 | 557.5 | 77.5 | 137 | 4 | AAG67102 | Aag67102 | Amino aci |
| 24 | 557.5 | 77.5 | 137 | 4 | AAG64775 | Aag64775 | Mouse ant |
| 25 | 557.5 | 77.5 | 137 | 4 | AAG63393 | Aag63393 | Amino aci |
| 26 | 557.5 | 77.5 | 137 | 5 | ABB95208 | Abb95208 | Mouse joi |
| 27 | 557.5 | 77.5 | 137 | 6 | ABJ36667 | Abj36667 | Angiogene |
| 28 | 557.5 | 77.5 | 137 | 8 | ADO33883 | Ado33883 | Murine pa |
| 29 | 557   | 77.5 | 119 | 6 | ABP58271 | Abp58271 | Humanised |
| 30 | 557   | 77.5 | 449 | 6 | ABP58273 | Abp58273 | Humanised |
| 31 | 554.5 | 77.1 | 139 | 1 | AAP90480 | Aap90480 | Chimeric  |
| 32 | 553   | 76.9 | 158 | 8 | ADL27491 | Adl27491 | Amino aci |
| 33 | 551   | 76.6 | 119 | 6 | ABP58269 | Abp58269 | Humanised |
| 34 | 551   | 76.6 | 158 | 2 | AAW19579 | Aaw19579 | Mouse ant |
| 35 | 551   | 76.6 | 477 | 2 | AAR47450 | Aar47450 | T84.12 He |
| 36 | 551   | 76.6 | 477 | 2 | AAR47453 | Aar47453 | chiT84.12 |
| 37 | 550.5 | 76.6 | 141 | 8 | ADO43551 | Ado43551 | Amino aci |
| 38 | 549   | 76.4 | 140 | 2 | AAW21841 | Aaw21841 | Heavy cha |
| 39 | 549   | 76.4 | 247 | 2 | AAW11917 | Aaw11917 | Murine MA |
| 40 | 547.5 | 76.1 | 141 | 8 | ADO43555 | Ado43555 | Amino aci |
| 41 | 545   | 75.8 | 142 | 2 | AAR30882 | Aar30882 | Antibody  |
| 42 | 542   | 75.4 | 140 | 7 | ADC24966 | Adc24966 | Murine G2 |
| 43 | 542   | 75.4 | 140 | 7 | ADK51721 | Adk51721 | Murine G2 |
| 44 | 539   | 75.0 | 136 | 2 | AAR06251 | Aar06251 | Variable  |
| 45 | 539   | 75.0 | 138 | 3 | AAV32406 | Aay32406 | Mouse ant |

# ALIGNMENTS

## RESULT 1

ABG76924

ID ABG76924 standard; protein; 138 AA.

XX

AC ABG76924;

XX

DT 05-NOV-2002 (first entry)

XX

DE Mouse 3D6 VH protein.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX  
 OS Mus musculus...  
 XX  
 PN WO200246237-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 06-DEC-2001; 2001WO-US046587.  
 XX  
 PR 06-DEC-2000; 2000US-0251892P.  
 XX  
 PA (NEUR-) NEURALAB LTD.  
 PA (AMHP ) WYETH.  
 XX  
 PI Basi G, Saldanha J, Yednock T;  
 XX  
 DR WPI; 2002-519658/55.  
 DR N-PSDB; ABS59427.  
 XX  
 PT Novel light/heavy chain of humanized immunoglobulin for treating  
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity  
 PT determining regions and variable framework region from human acceptor  
 PT immunoglobulin.  
 XX  
 PS Claim 68; Fig 2; 17lpp; English.  
 XX  
 CC The present invention relates to new humanized immunoglobulin (Ig) light  
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity  
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,  
 CC and variable framework region from human acceptor Ig LC or HC sequence.  
 CC The invention is useful for preventing or treating an amyloidogenic  
 CC disease or Alzheimer's disease in a patient. The invention is also useful  
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid  
 CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or  
 CC variable heavy (VH) chain protein of the invention  
 XX  
 SQ Sequence 138 AA;

Query Match 99.9%; Score 718; DB 5; Length 138;  
 Best Local Similarity 99.3%; Pred. No. 7e-57;  
 Matches 137; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS | 60  |
|    |     |   |     |
| Db | 1   | MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS | 60  |
| Qy | 61  | DKRLEWVASIRSGGGRYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH | 120 |
|    |     |   |     |
| Db | 61  | DKRLEWVASIRSGGGRYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH | 120 |
| Qy | 121 | YSGSSDYWGQGTITVTVSS   | 138 |
|    |     |   |     |
| Db | 121 | YSGSSDYWGQGTITVTVSS   | 138 |

RESULT 2  
 ABG76928

ID ABG76928 standard; protein; 138 AA.  
 XX  
 AC ABG76928;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Humanised 3D6 heavy chain variable region #1.  
 XX  
 KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;  
 KW variable region complementarity determining region; 3D6; 10D5;  
 KW variable framework region; amyloidogenic disease; Alzheimer's disease;  
 KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;  
 KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;  
 KW Abeta.  
 XX  
 OS Homo sapiens.  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 PN WO200246237-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 06-DEC-2001; 2001WO-US046587.  
 XX  
 PR 06-DEC-2000; 2000US-0251892P.  
 XX  
 PA (NEUR-) NEURALAB LTD.  
 PA (AMHP ) WYETH.  
 XX  
 PI Basi G, Saldanha J, Yednock T;  
 XX  
 DR WPI; 2002-519658/55.  
 XX  
 PT Novel light/heavy chain of humanized immunoglobulin for treating  
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity  
 PT determining regions and variable framework region from human acceptor  
 PT immunoglobulin.  
 XX  
 PS Claim 54; Page 155; 171pp; English.  
 XX  
 CC The present invention relates to new humanized immunoglobulin (Ig) light  
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity  
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,  
 CC and variable framework region from human acceptor Ig LC or HC sequence.  
 CC The invention is useful for preventing or treating an amyloidogenic  
 CC disease or Alzheimer's disease in a patient. The invention is also useful  
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid  
 CC sequence represents a humanized 3D6 variable light (VL) chain or variable  
 CC heavy (VH) chain protein of the invention  
 XX  
 SQ Sequence 138 AA;

Query Match 90.7%; Score 652; DB 5; Length 138;  
 Best Local Similarity 89.1%; Pred. No. 6.2e-51;  
 Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;



PI Tsurushita N, Vasquez M;  
 XX  
 DR WPI; 2003-183835/18.  
 DR N-PSDB; ABZ24633, ABZ24635.  
 XX  
 PT New humanized forms of mouse 3D6 antibodies, useful for treating Down's  
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral  
 PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta  
 PT plaque in the brain.  
 XX  
 PS Disclosure; Page 13-14; 54pp; English.  
 XX  
 CC The present sequence is that of a preferred heavy chain of a humanised  
 CC antibody of the present invention. In the variable region of this  
 CC sequence, the complementarity determining regions (CDRs) originate from  
 CC murine monoclonal antibody 3D6 and the framework region from human  
 CC germline VH segment DP-45 and J segment JH4. Novel humanised antibodies  
 CC of the invention have CDRs from 3D6 and human framework sequences. These  
 CC humanised antibodies have binding affinities (affinity and epitope  
 CC location) approximately the same as those of the mouse 3D6 antibody. The  
 CC invention includes antibodies, single chain antibodies, and their  
 CC fragments, as well as nucleotide sequences, vectors, transformed host  
 CC cells, and methods of using the humanised antibody to treat, prevent,  
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology  
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or  
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or  
 CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise  
 CC OS field)  
 XX  
 SQ Sequence 468 AA;

Query Match 90.5%; Score 651; DB 6; Length 468;  
 Best Local Similarity 89.1%; Pred. No. 3e-50;  
 Matches 123; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 ||||||||||||||||:||||||:| ||:|||| ||||||||||||  
 Db 1 MNFGLSLIFLVVLKGVQCEVQLVESGGGLVQPGGSLRLSCAGSGFTFSNYGMSWVRQAP 60  
  
 Qy 61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120  
 | ||||||||||||||||||||||||||||:||||:|::|||:||||||  
 Db 61 GKGLEWVASIRSGGGRITYSDNVKGRFTISRENAKNSLYLQMNSLRAEDTAVYYCVRYDH 120  
  
 Qy 121 YGSSDYWGQGTTLTVSS 138  
 ||||||||| ||||  
 Db 121 YGSSDYWGQGTTLTVSS 138

RESULT 4  
 ABG76932  
 ID ABG76932 standard; protein; 138 AA.  
 XX  
 AC ABG76932;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Humanised 3D6 heavy chain variable region #2.



Qy 121 YSGSSDYWGQGTTVTVSS 138  
|||||  
Db 121 YSGSSDYWGQGTTLVTVSS 138

RESULT 5

ABG74243

ID ABG74243 standard; protein; 133 AA.

XX

AC ABG74243;

XX

DT 22-APR-2003 (first entry)

XX

DE Mouse antibody 3D8 heavy chain variable region.

XX

KW T-cell receptor; cytostatic; dermatological; neuroprotective;

KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

KW 3E11; prostate-specific membrane antigen; zeta signalling chain;

KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

KW small cell lung cancer; heavy chain variable region; mouse.

XX

OS Mus sp.

XX

PN US2002132983-A1.

XX

PD 19-SEP-2002.

XX

PF 10-DEC-2001; 2001US-00006773.

XX

PR 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX

PA (JUNG/) JUNGHANS R P.

XX

PI Junghans RP;

XX

DR WPI; 2003-208946/20.

DR N-PSDB; ABX16569.

XX

PT New chimeric molecule useful in treating patients with disorders, such as

PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer

PT comprises GD3 and/or PSMA binding domains of antibody.

XX

PS Disclosure; Page 12; 35pp; English.

XX

CC The invention relates to a chimaeric molecule comprising the GD3

CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3

CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)

CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene

CC sequences, the zeta signalling chain of the T cell receptor and an

CC intervening CD8alpha hinge in which cysteine residues have been mutated.

CC The chimaeric molecules expressed in T cells or NK cells or other

CC effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),

CC and/or together with each other or with heterologous constructs to engage

CC additional stimulatory and functional properties of the effector cells to

CC enhance the antitumour therapeutic efficacy (claimed). They are  
CC particularly useful in disorders including melanoma, neuroendocrine  
CC tumours and prostate and small cell lung cancer. The present sequence  
CC represents the mouse antibody 3D8 heavy chain variable region  
XX  
SQ Sequence 133 AA;

Query Match 84.8%; Score 609.5; DB 6; Length 133;  
Best Local Similarity 87.0%; Pred. No. 4e-47;  
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||:|||||
Db      1 MNFGLSLIFLVVLKGVQCEVKVVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60

Qy     61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          ||| ||| |:|:|||||
Db     61 DKRLEWVASISSGGDSTFYADNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCARDL 120

Qy    121 YGSSTDYWGQGTTVTVSS 138
          :: |||:||||
Db    121 FN-----WGQGTTLTVSS 133
```

#### RESULT 6

ABG74247

ID ABG74247 standard; protein; 139 AA.

XX

AC ABG74247;

XX

DT 22-APR-2003 (first entry)

XX

DE Mouse antibody 3E11 heavy chain variable region.

XX

KW T-cell receptor; cytostatic; dermatological; neuroprotective;

KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

KW 3E11; prostate-specific membrane antigen; zeta signalling chain;

KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

KW small cell lung cancer; heavy chain variable region; mouse.

XX

OS Mus sp.

XX

PN US2002132983-A1.

XX

PD 19-SEP-2002.

XX

PF 10-DEC-2001; 2001US-00006773.

XX

PR 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX

PA (JUNG/) JUNGHANS R P.

XX

PI Junghans RP;

XX

DR WPI; 2003-208946/20.

DR N-PSDB; ABX16573.



KW Crohn's disease; diabetes mellitus; antibody; mouse.  
 XX  
 OS Mus sp.  
 XX  
 PN WO2003037913-A2.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 01-NOV-2002; 2002WO-US035333.  
 XX  
 PR 01-NOV-2001; 2001US-0346402P.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;  
 XX  
 DR WPI; 2003-441350/41.  
 DR N-PSDB; AAL60477.  
 XX  
 PT New purified antibody that specifically binds a TNF-related apoptosis-  
 PT inducing ligand receptor DR4 or DR5, useful for treating cancer,  
 PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or  
 PT rheumatoid arthritis.  
 XX  
 PS Example 16; Page 224-225; 251pp; English.  
 XX  
 CC The invention relates to an antibody that specifically binds a tumour  
 CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
 CC DR4 or DR5. Antibodies of the invention are useful for selectively  
 CC inducing apoptosis in target cells expressing DR4, for inhibiting  
 CC proliferation of target cells expressing DR4 or for treating cancer,  
 CC inflammatory disease or autoimmune disease in a subject e.g. systemic  
 CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-  
 CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple  
 CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or  
 CC glomerular nephritis. The present sequence is mouse anti-human DR5  
 CC antibody (TRA-8) heavy chain  
 XX  
 SQ Sequence 462 AA;

Query Match 80.4%; Score 578; DB 6; Length 462;  
 Best Local Similarity 81.2%; Pred. No. 1.1e-43;  
 Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 ||||||||||||||||||| ||||||||||| ||||||||||| |||||  
 Db 1 MNFGLSLIFLVLVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60  
 Qy 61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120  
 :|||||||:| ||| ||| |:|||||||:|||||||:|||||:| |  
 Db 61 EKRLEWVATISSGGSYTYYPDSVKGRFTISRDNKNTLYLQMSSLRSED'TAMYYCARRGD 120  
 Qy 121 YSGSSDYWGQGT'TVTVSS 138  
 ::|||||||:|||||  
 Db 121 SMITTDYWGQGT'TLVSS 138

RESULT 8

ADJ79787

ID ADJ79787 standard; protein; 462 AA.

XX

AC ADJ79787;

XX

DT 06-MAY-2004 (first entry)

XX

DE TRA-8 antibody heavy chain.

XX

KW nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;

KW antiallergic; antiinflammatory; antidiabetic; haemostatic;

KW neuroprotective; antiinfertility; immunosuppressive; dermatological;

KW antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;

KW proliferation;

KW tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;

KW TRAIL; synovial cell; lymphocyte; neutrophil;

KW systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;

KW graft-versus-host disease; Sjogren's syndrome; pernicious anemia;

KW Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;

KW autoimmune hemolytic anemia; sterility; myasthenia gravis;

KW multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;

KW thrombopenia purpura; insulin dependent diabetes mellitus; allergy;

KW asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;

KW glomerular nephritis; hypoplastic anemia.

XX

OS Homo sapiens.

XX

PN WO2003038043-A2.

XX

PD 08-MAY-2003.

XX

PF 25-OCT-2002; 2002WO-US034420.

XX

PR 01-NOV-2001; 2001US-0346402P.

PR 24-JUN-2002; 2002US-0391478P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;

PI Lobuglio AF, Buchsbaum DJ;

XX

DR WPI; 2003-421518/39.

XX

PT Inducing apoptosis and inhibiting proliferation of target cells

PT expressing DR5, by contacting the target cell with an antibody that binds

PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic

PT agents.

XX

PS Example 16; SEQ ID NO 23; 274pp; English.

XX

CC The invention relates to a method of selectively inducing apoptosis in

CC and inhibiting (M1) proliferation of target cells expressing DR5,

CC comprising contacting the cell with an antibody that specifically binds

CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)

CC receptor DR5, where the antibody, in its soluble form, has in vivo and in

CC vitro apoptosis-inducing activity in the cell expressing DR5, and

CC contacting the cell with one or more therapeutic agents. M1 is useful for  
 CC inducing apoptosis in target cell and inhibiting proliferation of target  
 CC cell expressing DR5, where the target cell is an abnormally proliferating  
 CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated  
 CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected  
 CC cell. M2 is useful for treating a subject having inflammatory and  
 CC autoimmune diseases. The inflammatory or autoimmune disease are selected  
 CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid  
 CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious  
 CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,  
 CC thrombopenia purpura, insulin dependent diabetes mellitus, allergy,  
 CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerular nephritis, and hypoplastic anemia. This sequence represents a  
 CC protein used in the method of the invention.

XX

SQ Sequence 462 AA;

Query Match 80.4%; Score 578; DB 7; Length 462;  
 Best Local Similarity 81.2%; Pred. No. 1.1e-43;  
 Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |||||||||||||||| |||||||||||| |||||||||||||:| |||||  
 Db 1 MNFGLSLIFLVLVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60  
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRETISRANAKNTLYLQMSLKS EDTALYYCVRYDH 120  
 :||||||:| ||| ||| |:|||||||:|||||||||||:||||:| |  
 Db 61 EKRLEWVATISSGGSYTYYPDSVKGRETISRDNAKNTLYLQMSLRS EDTAMYYCARRGD 120  
 Qy 121 YSGSSDYWGQGT TVTVSS 138  
 ::|||||||:||||  
 Db 121 SMITTDYWGQGT TLTVSS 138

# RESULT 9

AAU72801

ID AAU72801 standard; protein; 464 AA.

XX

AC AAU72801;

XX

DT 26-FEB-2002 (first entry)

XX

DE TRA-8 heavy chain.

XX

KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;

KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;

KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;

KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;

KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;

KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;

KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;

KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.

XX

OS Mus musculus.

XX

```

PN WO200183560-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014151.
XX
PR 02-MAY-2000; 2000US-0201344P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
DR WPI; 2002-049338/06.
DR N-PSDB; AAS97062.
XX
PT Novel antibody specific for tumor necrosis factor-related apoptosis-
PT inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
PS Claim 26; Page 198-199; 229pp; English.
XX
CC The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus
CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC breast tissue. Peptides used to design primers for isolating heavy and
CC light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are
CC shown in AAU72799 and AAU72800
XX
SQ Sequence 464 AA;

Query Match          80.4%; Score 578; DB 5; Length 464;
Best Local Similarity 81.2%; Pred. No. 1.le-43;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSAASGFTFSNYGMSWVRQNS 60
        ||| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db      1 MNFGLSLIFLVLVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRTISRNAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        :||| | |:| | |:| | | |:| | | |:| | | |:| | | |
Db     61 EKRLEWVATISSGGSYTYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDAMYCARRGD 120

Qy    121 YSGSSDYWGQGTTVTTVSS 138

```

Db                   ::|||||||:||||  
121 SMITTDYWGQGTTLTVSS 138

RESULT 10

AAR20064

ID   AAR20064 standard; protein; 138 AA.

XX

AC   AAR20064;

XX

DT   24-OCT-2003   (revised)

DT   25-MAR-2003   (revised)

DT   27-MAR-1992   (first entry)

XX

DE   MRK16-H chain.

XX

KW   Monoclonal antibody; light; heavy; chain; cancer; drug resistance.

XX

OS   Homo; sapiens.

OS   Mus musculus.

OS   Chimeric.

XX

PN   JP03254691-A.

XX

PD   13-NOV-1991.

XX

PF   02-MAR-1990;   90JP-00051563.

XX

PR   02-MAR-1990;   90JP-00051563.

XX

PA   (GANK-) ZH GAN KENKYUKAI.

PA   (FUJI-) FUJITA GAKUEN GH.

PA   (NICA-) JAPAN FOUND CANCER RES.

XX

DR   WPI; 1992-002461/01.

DR   N-PSDB; AAQ20070.

XX

PT   Chimera antibody against drug resistant cancer - comprises variable  
PT   region homologous to region in mouse monoclonal antibody and constant  
PT   region homologous to region in human immunoglobulin.

XX

PS   Disclosure; Fig 4; 20pp; Japanese.

XX

CC   A chimeric antibody against drug-resistant cancer consists of (1) a  
CC   variable region having an amino acid sequence homologous to a variable  
CC   region in the mouse monoclonal antibody against drug- resistance and (2)  
CC   a constant region having an amino acid sequence homologous to the  
CC   constant region in human immunoglobulin. The chimeric antibody  
CC   selectively inhibits the growth of cancer cells showing drug resistance  
CC   or enhances the sensitivity to the drug. The antibody is very low in  
CC   immunogenicity. The MRK16-L chain is shown in AAQ20071. (Updated on 25-  
CC   MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS  
CC   field)

XX

SQ   Sequence 138 AA;

Query Match

79.7%;   Score 573;   DB 2;   Length 138;

Best Local Similarity 80.4%; Pred. No. 8.1e-44;  
Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||:||||| ||||| |||||:| |||||
Db      1 MNFGLSLIFLVLILKGVQCEVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          :|||||:| |||| ||| |:|||||:|||| |||||:||||| ||
Db     61 EKRLEWVATISSGGGNTYYPDVSKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYR 120

Qy    121 YSGSSDYWGQGTTVTVSS 138
          | |||| |||:
Db    121 YEAWFASWGQGTLLVTVSA 138
```

RESULT 11

ABB79730

ID ABB79730 standard; protein; 144 AA.

XX

AC ABB79730;

XX

DT 29-OCT-2002 (first entry)

XX

DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.

XX

KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;  
KW antibody; anticaries; transgenic plant; transgenic animal; caries;  
KW immunotherapy; therapy.

XX

OS Mus musculus.

XX

PN US2002068066-A1.

XX

PD 06-JUN-2002.

XX

PF 15-JUN-2001; 2001US-00881823.

XX

PR 20-AUG-1999; 99US-00378577.

XX

PA (SHIW/) SHI W.

PA (MORR/) MORRISON S L.

PA (TRIN/) TRINH K.

PA (WIMS/) WIMS L.

PA (CHEN/) CHEN L.

PA (ANDE/) ANDERSON M H.

XX

PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX

DR WPI; 2002-565838/60.

DR N-PSDB; ABN84611.

XX

PT Treatment and prevention of dental caries in mammals, in particular  
PT humans by orally administering genetically engineered or purified  
PT antibodies that bind to surface antigens of carcinogenic organisms.

XX

PS Claim 14; Fig 3B; 30pp; English.

XX  
 CC The present sequence is the protein sequence of the heavy chain variable  
 CC region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds  
 CC specifically to the surface antigens of cariogenic type c Streptococcus  
 CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC  
 CC HB 12558) hybridoma cells. In an example from the invention, chimeric  
 CC monoclonal antibody TEFÉ was produced comprising SWLA3 variable regions  
 CC and human antibody constant regions. Such chimeric monoclonal antibodies  
 CC can be used to prevent or treat dental caries in humans. The antibodies  
 CC engage the effector apparatus of the human immune system when they bind  
 CC cariogenic organisms, resulting in their destruction. The chimeric  
 CC antibodies may be produced in edible plants, in transgenic animals, or in  
 CC chicken eggs for oral ingestion  
 XX  
 SQ Sequence 144 AA;

Query Match 79.1%; Score 569; DB 5; Length 144;  
 Best Local Similarity 78.2%; Pred. No. 2e-43;  
 Matches 111; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |:||||:|||| |||||:||||||| || ||||||||:| |||||  
 Db 1 MDFGLSLVFLVLTLLKGVQCDVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMSWVRQTP 60  
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRANAKNTLYLQMSLKSSEDALYYCVR--- 117  
 :||||||| ||| ||| |:|||||||:|||||||:||||||:||| |  
 Db 61 EKRLEWVASISSGGTYTYPDSVKGRFTISRDNANAKNTLYLQMTSLKSEDTAMYCYCSRDDG 120  
 Qy 118 -YDHYSGSSDYWGQGTTVTVSS 138  
 | | : |||||:|||||  
 Db 121 SYGSYYYAMDYWGQGTSVTVSS 142

# RESULT 12

AAR30480

ID AAR30480 standard; protein; 139 AA.

XX

AC AAR30480;

XX

DT 06-MAY-1993 (first entry)

XX

DE hCEA specific mouse heavy chain variable chain region.

XX

KW Chimeric antibody; human cancer embryonal antigen; treatment; diagnosis;  
 KW cancer.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /note= "signal peptide"

FT Protein 20. .139

FT /note= "mature peptide"

XX

PN JP04330295-A.

XX

PD 18-NOV-1992.



KW osteoarthritis; graft versus host disease; autoimmune disease;  
 KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;  
 KW myasthenia gravis.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .19  
 FT /label= Signal\_peptide  
 FT Protein 20. .140  
 FT /label= Mature\_VH  
 FT Region 50. .54  
 FT /label= Complementarity\_determining\_region  
 FT /note= "This region is specifically claimed in claim 3"  
 FT Region 69. .85  
 FT /label= Complementarity\_determining\_region  
 FT /note= "This region is specifically claimed in claim 3"  
 FT Region 118. .129  
 FT /label= Complementarity\_determining\_region  
 FT /note= "This region is specifically claimed in claim 3"  
 XX  
 PN US2002010320-A1.  
 XX  
 PD 24-JAN-2002.  
 XX  
 PF 05-APR-1999; 99US-00286240.  
 XX  
 PR 05-APR-1999; 99US-00286240.  
 XX  
 PA (FETT/) FETT J W.  
 XX  
 PI Fett JW;  
 XX  
 DR WPI; 2002-187790/24.  
 DR N-PSDB; ABK15270.  
 XX  
 PT New antibody immunologically reactive to angiogenin useful for inhibiting  
 PT angiogenesis and for treating conditions associated with abnormal  
 PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid  
 PT arthritis.  
 XX  
 PS Claim 6; Page 14; 20pp; English.  
 XX  
 CC The invention relates to an antibody immunologically reactive to  
 CC angiogenin or a fragment of angiogenin comprising light and heavy chain  
 CC nonhuman-derived complementarity determining regions having a binding  
 CC affinity to the angiogenin or its fragment in combination with human  
 CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also  
 CC included are an expression vector comprising a nucleic acid encoding the  
 CC antibody and a host cell transformed with the vector. The antibody or its  
 CC fragment is useful for inhibiting the angiogenic activity of angiogenin.  
 CC The antibody is useful for treating a tumour in humans, by inhibiting,  
 CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the  
 CC ability of circulating tumour cell to form a vascularised tumour mass.  
 CC The antibody is useful for treating a mammal with abnormal or unwanted  
 CC angiogenesis, including cancer, and other diseases mediated by  
 CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,



XX  
 PN JP04234987-A.  
 XX  
 PD 24-AUG-1992.  
 XX  
 PF 28-DEC-1990; 90JP-00408810.  
 XX  
 PR 28-DEC-1990; 90JP-00408810.  
 XX  
 PA (MITU ) MITSUBISHI KASEI CORP.  
 XX  
 DR WPI; 1992-327631/40.  
 DR N-PSDB; AAQ28746.  
 XX  
 PT New DNA fragments encoding variable regions of ABS specific for human CEA  
 PT - for diagnosing and monitoring tumours, as tumour markers and for  
 PT treatment of tumours.  
 XX  
 PS Disclosure; Fig 1; 7pp; Japanese.  
 XX  
 CC The anti-CEA murine monoclonal antibody heavy chain variable region was  
 CC obtd. by screening a cDNA library prepd. from mRNA obtd. from hybridomas  
 CC producing anti-CEA-specific antibodies with a probe based on the constant  
 CC region of the H-chain. The antibodies reacts specifically with human CEA  
 CC and are useful as a diagnostic agents, as tumour markers for digestive  
 CC organs, for diagnosis of malignant tumours; for monitering after cancer  
 CC operations, to follow up bloodless therapy or as therapeutic agents in  
 CC passive immune therapy and targetting therapy. See also AAR27054  
 XX  
 SQ Sequence 139 AA;

Query Match 78.4%; Score 564; DB 2; Length 139;  
 Best Local Similarity 79.9%; Pred. No. 5.3e-43;  
 Matches 111; Conservative 11; Mismatches 15; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |||| -|||||  
 Db 1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP 60  
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVRYDH 120  
 :||||||| | | ||| |:|||||||:|:| |||||:|:|:| | :  
 Db 61 EKRLEWVASITSDGS-TYYPDSVKGRFTISRDNARNILYLQMSSLRSEETAMYYCARVHY 119  
 Qy 121 Y-SGSSDYWGQGTTVTVSS 138  
 | | : |||||:|||||  
 Db 120 YDSPAMDYWGQGTSTVTVSS 138

# RESULT 15

AAU76133

ID AAU76133 standard; protein; 140 AA.

XX

AC AAU76133;

XX

DT 08-MAY-2002 (first entry)

XX

DE Mouse mAb 26-2F heavy chain variable region mutant E59Y.

XX  
 KW Mouse; angiogenin; angiogenesis; tumour; cancer; retinopathy;  
 KW ocular neovascular disease; vitamin A deficiency; syphilis;  
 KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;  
 KW sickle cell anaemia; Paget's disease; mycobacterial infection;  
 KW osteoarthritis; graft versus host disease; autoimmune disease;  
 KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;  
 KW myasthenia gravis; mutant; mutein; monoclonal antibody; 26-2F;  
 KW heavy chain variable region; E59Y.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .19  
 FT /label= Signal\_peptide  
 FT Protein 20. .140  
 FT /label= Mature\_VH  
 FT Misc-difference 59  
 FT /note= "Wild-type Glu substituted by Tyr"  
 XX  
 PN US2002010320-A1.  
 XX  
 PD 24-JAN-2002.  
 XX  
 PF 05-APR-1999; 99US-00286240.  
 XX  
 PR 05-APR-1999; 99US-00286240.  
 XX  
 PA (FETT/) FETT J W.  
 XX  
 PI Fett JW;  
 XX  
 DR WPI; 2002-187790/24.  
 XX  
 PT New antibody immunologically reactive to angiogenin useful for inhibiting  
 PT angiogenesis and for treating conditions associated with abnormal  
 PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid  
 PT arthritis.  
 XX  
 PS Claim 11; Page; 20pp; English.  
 XX  
 CC The invention relates to an antibody immunologically reactive to  
 CC angiogenin or a fragment of angiogenin comprising light and heavy chain  
 CC nonhuman-derived complementarity determining regions having a binding  
 CC affinity to the angiogenin or its fragment in combination with human  
 CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also  
 CC included are an expression vector comprising a nucleic acid encoding the  
 CC antibody and a host cell transformed with the vector. The antibody or its  
 CC fragment is useful for inhibiting the angiogenic activity of angiogenin.  
 CC The antibody is useful for treating a tumour in humans, by inhibiting,  
 CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the  
 CC ability of circulating tumour cell to form a vascularised tumour mass.  
 CC The antibody is useful for treating a mammal with abnormal or unwanted  
 CC angiogenesis, including cancer, and other diseases mediated by  
 CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,  
 CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma

CC and retrolental fibroplasia, and other diseases associated with corneal  
 CC neovascularisation including epidemic keratoconjunctivitis, vitamin A  
 CC deficiency, contact lens overwear, atopic keratitis, superior limbic  
 CC keratitis, syphilis, mycobacteria infections, lipid degeneration,  
 CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex  
 CC infections, herpes zoster infections, protozoan infections, Kaposi's  
 CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,  
 CC Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal  
 CC graft rejection. Diseases associated with retinal/choroidal  
 CC neovascularisation include macular degeneration, sickle cell anaemia,  
 CC sarcoid, Paget's disease, mycobacterial infections, Bechets disease,  
 CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host  
 CC disease, transplant rejection, autoimmune diseases such as type I  
 CC diabetes, multiple sclerosis, systemic lupus erythematosus, and  
 CC myasthenia gravis. The present sequence represents the E59Y mutant of the  
 CC mouse monoclonal antibody 26-2F light chain variable region. Note: The  
 CC present sequence is not shown in the specification but was created by the  
 CC indexer using the sequence appearing as AAU76122 and the information in  
 CC the claims

XX

SQ Sequence 140 AA;

Query Match 78.4%; Score 564; DB 5; Length 140;  
 Best Local Similarity 79.3%; Pred. No. 5.3e-43;  
 Matches 111; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |:||||:||||:||||||| ||||||||| |||||||||:| |||||  
 Db 1 MDFGLSWVFLVLILKGVQCEVWLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQYP 60  
 Qy 61 DKRLEWVASIRSGGGRYYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVRY-D 119  
 :|||||||:| ||| || |:|||||||: |||||||||:||||||| | |  
 Db 61 EKRLEWVATISSGGGNTYYPDSVKGRFTISRDIKNTLYLQMSSLRSEDTALYYCTRLGD 120  
 Qy 120 H-YSGSSDYWGQGTTVTVSS 138  
 : |: : ||||||:|||||  
 Db 121 YGYAYTMDYWGGTTSVTVSS 140

Search completed: December 13, 2004, 19:13:31  
 Job time : 125.022 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:05:17 ; Search time 28.6222 Seconds  
(without alignments)  
319.748 Million cell updates/sec

Title: US-10-010-942B-4  
Perfect score: 719  
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result<br>No. | %<br>Query |              | DB  | ID | Description       |
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|               | Score      | Match Length |     |    |                   |
| 1             | 566.5      | 78.8         | 135 | 3  | US-08-579-378A-16 |
| 2             | 563        | 78.3         | 138 | 2  | US-08-379-057-14  |
| 3             | 551        | 76.6         | 158 | 2  | US-08-653-402B-6  |
| 4             | 549        | 76.4         | 140 | 3  | US-08-836-561-23  |
| 5             | 549        | 76.4         | 140 | 4  | US-09-434-122-23  |
| 6             | 549        | 76.4         | 247 | 5  | PCT-US94-07659-2  |
| 7             | 545.5      | 75.9         | 135 | 3  | US-08-579-378A-20 |
| 8             | 541        | 75.2         | 136 | 3  | US-08-976-183A-33 |
| 9             | 540        | 75.1         | 136 | 3  | US-08-976-183A-31 |
| 10            | 537        | 74.7         | 136 | 3  | US-08-976-183A-32 |
| 11            | 536        | 74.5         | 136 | 3  | US-08-976-183A-34 |

|    |       |      |     |   |                   |                   |
|----|-------|------|-----|---|-------------------|-------------------|
| 12 | 535   | 74.4 | 136 | 1 | US-08-253-877C-57 | Sequence 57, Appl |
| 13 | 535   | 74.4 | 136 | 2 | US-08-452-164A-57 | Sequence 57, Appl |
| 14 | 535   | 74.4 | 138 | 1 | US-08-053-171-7   | Sequence 7, Appli |
| 15 | 535   | 74.4 | 138 | 1 | US-08-053-171-11  | Sequence 11, Appl |
| 16 | 535   | 74.4 | 158 | 2 | US-08-653-402B-10 | Sequence 10, Appl |
| 17 | 514.5 | 71.6 | 139 | 1 | US-08-129-930B-96 | Sequence 96, Appl |
| 18 | 514.5 | 71.6 | 139 | 3 | US-08-134-346A-51 | Sequence 51, Appl |
| 19 | 514.5 | 71.6 | 139 | 3 | US-08-976-288A-96 | Sequence 96, Appl |
| 20 | 513   | 71.3 | 170 | 2 | US-08-652-558-40  | Sequence 40, Appl |
| 21 | 512.5 | 71.3 | 159 | 2 | US-08-653-402B-2  | Sequence 2, Appli |
| 22 | 497.5 | 69.2 | 255 | 2 | US-07-690-192-4   | Sequence 4, Appli |
| 23 | 494.5 | 68.8 | 463 | 4 | US-09-472-087-1   | Sequence 1, Appli |
| 24 | 494.5 | 68.8 | 463 | 4 | US-09-472-087-63  | Sequence 63, Appl |
| 25 | 494.5 | 68.8 | 463 | 4 | US-09-472-087-64  | Sequence 64, Appl |
| 26 | 493   | 68.6 | 464 | 4 | US-09-472-087-2   | Sequence 2, Appli |
| 27 | 493   | 68.6 | 464 | 4 | US-09-472-087-66  | Sequence 66, Appl |
| 28 | 490.5 | 68.2 | 135 | 5 | PCT-US95-07302-8  | Sequence 8, Appli |
| 29 | 486   | 67.6 | 130 | 4 | US-09-225-322B-8  | Sequence 8, Appli |
| 30 | 486   | 67.6 | 130 | 4 | US-09-764-304-8   | Sequence 8, Appli |
| 31 | 484.5 | 67.4 | 122 | 1 | US-07-634-278-48  | Sequence 48, Appl |
| 32 | 484.5 | 67.4 | 122 | 1 | US-08-477-728-48  | Sequence 48, Appl |
| 33 | 484.5 | 67.4 | 122 | 1 | US-08-474-040-48  | Sequence 48, Appl |
| 34 | 484.5 | 67.4 | 122 | 1 | US-08-487-200-48  | Sequence 48, Appl |
| 35 | 484.5 | 67.4 | 122 | 3 | US-08-484-537-48  | Sequence 48, Appl |
| 36 | 484   | 67.3 | 130 | 4 | US-09-225-322B-18 | Sequence 18, Appl |
| 37 | 484   | 67.3 | 130 | 4 | US-09-764-304-18  | Sequence 18, Appl |
| 38 | 482.5 | 67.1 | 135 | 3 | US-08-619-491-8   | Sequence 8, Appli |
| 39 | 482.5 | 67.1 | 463 | 4 | US-09-472-087-4   | Sequence 4, Appli |
| 40 | 482.5 | 67.1 | 463 | 4 | US-09-472-087-68  | Sequence 68, Appl |
| 41 | 480.5 | 66.8 | 456 | 4 | US-09-495-880A-11 | Sequence 11, Appl |
| 42 | 478.5 | 66.6 | 135 | 3 | US-08-619-491-4   | Sequence 4, Appli |
| 43 | 478.5 | 66.6 | 135 | 5 | PCT-US95-07302-4  | Sequence 4, Appli |
| 44 | 477   | 66.3 | 239 | 2 | US-08-553-497A-18 | Sequence 18, Appl |
| 45 | 475   | 66.1 | 123 | 3 | US-09-344-587-13  | Sequence 13, Appl |

#### ALIGNMENTS

#### RESULT 1

US-08-579-378A-16

; Sequence 16, Application US/08579378A

; Patent No. 6210671

; GENERAL INFORMATION:

; APPLICANT: Co, Man Sung

; TITLE OF INVENTION: Humanized Antibodies Reactive with

; TITLE OF INVENTION: L-Selectin

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One MarketPlaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

```

;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/579,378A
;     FILING DATE:  27-DEC-1995
;     CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/160,074
;     FILING DATE:  30-NOV-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/983,946
;     FILING DATE:  01-DEC-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP 95112895.8
;     FILING DATE:  17-AUG-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP 95114696.8
;     FILING DATE:  19-SEP-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Liebescheutz, Joe O.
;     REGISTRATION NUMBER:  37,505
;     REFERENCE/DOCKET NUMBER:  11823-002220
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415-326-2400
;     TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  135 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-579-378A-16

```

```

Query Match          78.8%;  Score 566.5;  DB 3;  Length 135;
Best Local Similarity 81.2%;  Pred. No. 1.4e-52;
Matches 112;  Conservative 8;  Mismatches 15;  Indels 3;  Gaps 2;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGSSLIFFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLACAASGFTFSTYAMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDALYYCVRYDH 120
      :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 EKRLEWVASI-STGGSTYYPDVSVKGRFTISRDNARNILYLQMSSLRSEDAMYYCAR--D 117

Qy    121 YSGSSDYWGQGTTTVTVSS 138
      || ||||| ||||| |||||
Db    118 YDGYFDYWQGTTTLTVSS 135

```

# RESULT 2

```

US-08-379-057-14
; Sequence 14, Application US/08379057
; Patent No. 5876950
; GENERAL INFORMATION:
;   APPLICANT:  Siadak, Anthony W.

```



RESULT 3

US-08-653-402B-6

; Sequence 6, Application US/08653402B

; Patent No. 5969107

; GENERAL INFORMATION:

; APPLICANT: CARCELLER, Ana

; APPLICANT: ROSELL, Elisabet

; APPLICANT: GOMEZ, Alicia

; APPLICANT: ADEN, Jaume

; APPLICANT: PIULATS, Jaume

; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an

; TITLE OF INVENTION: immune response against epidermal growth factor receptor.

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.

; STREET: 2200 Clarendon Boulevard, Suite 1400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/653,402B

; FILING DATE: 24-MAY-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95107967.2

; FILING DATE: 26-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lebovitz, Richard M.

; REGISTRATION NUMBER: 37,067

; REFERENCE/DOCKET NUMBER: MERCK 1781

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-243-6333

; TELEFAX: 703-243-6410

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 158 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-653-402B-6

Query Match 76.6%; Score 551; DB 2; Length 158;

Best Local Similarity 77.8%; Pred. No. 7.5e-51;

Matches 112; Conservative 9; Mismatches 17; Indels 6; Gaps 2;

Qy 1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

|:||||||||||| ||| |:||||||||||| | ||||||||||||| |||||

Db 1 MDFGLSLIFLVLVFKGVLCVDKLVESGGGLVKLGSLKLSCAASGFTFSNYMSWVRQTP 60

```

QY          61 DKRLEWVASIRSGGGRYYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVRY-- 118
           :|||:|:| | || ||| | |||||:||||| ||||| ||||| | :
Db          61 EKRLEFVAAINSNGGSTYYPTVKGRFTISRDNAKNTLYLQMSSLKSEDTALYYCARHRG 120

QY          119 ---DHYSG-SSDYWGQGTTVTVSS 138
           | | : |||||:|||||
Db          121 RDSSGYVGYAIDYWGOGTSVTVSS 144

```

US-08-836-561-23

; Patent No. 6018032

APPLICANT: KOIKE, Masamichi

APPLICANT: NAKAMURA, Kazuyasu

; APPLICANT: IIDA, Akihiro

; APPLICANT: ANAZAWA, Hideharu

; APPLICANT: HANAI, No. 6018032uo

; APPLICANT: TAKATSU, Kiyoshi

; TITLE OF INVENTION: Antibody Against Human

; TITLE OF INVENTION: Rece

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 A

; CITY: New York

STATE: NY

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

```

; OPERATING SYSTEM:  DOS

```

```
; SOFTWARE: FastSEQ Version 2.0
```

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,561

FILING DATE: 09-MAY-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 232384/95

FILING DATE: 11-SEP-1995

ATTORNEY/AGENT INFORMATION:

; NAME: Lawrence, III, Stanton T

REGISTRATION NUMBER: 25,736

REFERENCE/DOCKET NUMBER: 7005-115-999

: TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 140 amino acids

TYPE: amino acid

```
;      TOPOLOGY:   linear
;      MOLECULE TYPE:  protein
;      FRAGMENT TYPE:  internal
US-08-836-561-23
```

Query Match 76.4%; Score 549; DB 3; Length 140;  
Best Local Similarity 74.3%; Pred. No. 1e-50;  
Matches 104; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| | : ||||| : ||||| ||||| ||||| : ||| : ||| |
Db      1 MNFGLSLIFLALILKGVQCEVQLVESGGDLVKPGGSLKLSCAASGFTFSYDGMWIRQIS 60

Qy      61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        ||| ||||:| |||  :: |:|:||||:|:|:|||||:| | |||||:||| |
Db      61 DKRPEWVAAISSGGSYIHFPDSLKGRFTVSRDNAKNTLYLEMSGLKSEDTAMYYCARRGF 120

Qy      121 YSG--SSDYWGQGTTVTVSS 138
        |   : |||||:|||||
Db      121 YGNYRAMDYWGQTSVTVSS 140

```

## RESULT 5

US-09-434-122-23

```

; Sequence 23, Application US/09434122
; Patent No. 6538111

```

## ; GENERAL INFORMATION:

APPLICANT: KOIKE, Masamichi  
FURUYA, Akiko  
NAKAMURA, Kazuyasu  
IIDA, Akihiro  
ANAZAWA, Hideharu  
HANAI, No. 6538111uo  
TAKATSU, Kiyoshi

TITLE OF INVENTION: Antibody Against Human Interleukin-5  
Receptor Alpha Chain

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

```

;      ADDRESSEE: Pennie & Edmonds LLP
;      STREET: 1155 Avenue of the Americas
;      CITY: New York
;      STATE: NY
;      COUNTRY: USA
;      ZIP: 10036

```

COMPUTER READABLE FORM:

```

;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ Version 2.0

```

## ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/434,122  
FILING DATE: 05-No. 6538111-1999

## ; PRIOR APPLICATION DATA:

```

;      APPLICATION NUMBER: 08/836,561
;      FILING DATE: 09-MAY-1997
;      APPLICATION NUMBER: JP 232384/95
;      FILING DATE: 11-SEP-1995

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-434-122-23

```

```

Query Match          76.4%; Score 549; DB 4; Length 140;
Best Local Similarity 74.3%; Pred. No. 1e-50;
Matches 104; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGF*TFSNYGMWVRQNS 60
        ||||| | : ||||| : ||||| ||||| ||||| ||||| : || : || |
Db      1 MNFGLSLIFLALILKGVQCEVQLVESGGDLVKPGGSLKLSCAASGFTFSDYGMWIRQIS 60

Qy      61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        ||| ||||:| ||| : : ||: ||||: ||: ||||| : || ||||| : || |
Db      61 DKRPEWVAAISSGGSYIHFPDSLKGRFTVSRDNAKNTLYLEMSGLKSEDTAMYYCARRGF 120

Qy      121 YSG--SSDYWGQGT*TVTVSS 138
        | : ||||| : |||||
Db      121 YGNYRAMDYWGQGT*SVTVSS 140

```

# RESULT 6

PCT-US94-07659-2

; Sequence 2, Application PC/TUS9407659

## ; GENERAL INFORMATION:

```

; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

```

```

; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-2

```

```

Query Match          76.4%; Score 549; DB 5; Length 247;
Best Local Similarity 78.3%; Pred. No. 2.1e-50;
Matches 108; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| ||||| ||||:|| | ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGLRLIFLVLTLKGVKCEVHLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        :|||:||| | ||| || | ||||| ||||| ||||| ||||| ||||| |||||
Db     61 EKRLDWVAYISSGGGGTYPDTVKGRFTISRDNKNTLYLQMSSLKSEDTAMYHCARGGV 120

Qy    121 YSGSSDYWGQGTTVTVSS 138
        | | || |||||
Db    121 RRGYFDVWGAGTTTVTVSS 138

```

# RESULT 7

```

US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One MarketPlaza, Steuart Tower, Suite 2000

```

```

;   CITY:  San Francisco
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94105
;
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/579,378A
;   FILING DATE:  27-DEC-1995
;   CLASSIFICATION:  424
;
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/160,074
;   FILING DATE:  30-NOV-1993
;
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/983,946
;   FILING DATE:  01-DEC-1992
;
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  EP 95112895.8
;   FILING DATE:  17-AUG-1995
;
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  EP 95114696.8
;   FILING DATE:  19-SEP-1995
;
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Liebescheutz, Joe O.
;   REGISTRATION NUMBER:  37,505
;   REFERENCE/DOCKET NUMBER:  11823-002220
;
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-326-2400
;   TELEFAX:  415-326-2422
;
;   INFORMATION FOR SEQ ID NO:  20:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  135 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-579-378A-20

```

```

Query Match          75.9%;  Score 545.5;  DB 3;  Length 135;
Best Local Similarity 79.0%;  Pred. No. 2.3e-50;
Matches 109;  Conservative 9;  Mismatches 17;  Indels 3;  Gaps 2;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGSSLIFLVLVLKGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | ||||| | || || | : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 GKGLEWVASI-STGGSTYYPDVSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR--D 117

Qy    121 YSGSSDYWGQGTTVTVSS 138
      | | ||||| |||||
Db    118 YDGYFDYWGQGTTLTVSS 135

```

RESULT 8  
 US-08-976-183A-33  
 ; Sequence 33, Application US/08976183A  
 ; Patent No. 6307026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: King, David J.  
 ; APPLICANT: Adair, John R.  
 ; APPLICANT: Owens, Raymond J.  
 ; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33  
 ; TITLE OF INVENTION: ANTIGEN  
 ; NUMBER OF SEQUENCES: 55  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY & LARDNER  
 ; STREET: 3000 K. Street, N.W., Suite 500  
 ; CITY: Washington, D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/976,183A  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/595,848  
 ; FILING DATE: 02-FEB-1996  
 ; APPLICATION NUMBER: PCT/GB93/02529  
 ; FILING DATE: 10-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9225853.2  
 ; FILING DATE: 10-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 9315249.4  
 ; FILING DATE: 22-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bernhard D. Saxe  
 ; REGISTRATION NUMBER: 28,665  
 ; REFERENCE/DOCKET NUMBER: 40283/151/CARA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 672-5300  
 ; TELEFAX: (202) 672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 33:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 136 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-976-183A-33

Query Match 75.2%; Score 541; DB 3; Length 136;  
 Best Local Similarity 75.5%; Pred. No. 7.1e-50;  
 Matches 108; Conservative 10; Mismatches 13; Indels 12; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |||||:||||| ||||| |||||  
 Db 1 MNFGLSLIFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGRYYSDNVKGRTISRENAKNTLYLQMSSLKSEDTALYYC----- 115  
 :|||||:| ||| ||| |:|||||:|:|||||:|||||  
 Db 61 EKRLEWVATISSGGSYTYLDSVKGRTISRDSARNTLYLQMSSLRSEDTALYYCAPTTV 120

Qy 116 VRYDHYSGSSDYWGQTTTVTVSS 138  
 | : ||||| ||||:  
 Db 121 VPF-----AYWGQGTTLVTVSA 136

RESULT 9

US-08-976-183A-31

; Sequence 31, Application US/08976183A

; Patent No. 6307026

; GENERAL INFORMATION:

; APPLICANT: King, David J.

; APPLICANT: Adair, John R.

; APPLICANT: Owens, Raymond J.

; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

; TITLE OF INVENTION: ANTIGEN

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K. Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/976,183A

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/595,848

; FILING DATE: 02-FEB-1996

; APPLICATION NUMBER: PCT/GB93/02529

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9225853.2

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 9315249.4

; FILING DATE: 22-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Bernhard D. Saxe

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 40283/151/CARA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 136 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-976-183A-31

Query Match 75.1%; Score 540; DB 3; Length 136;  
 Best Local Similarity 74.8%; Pred. No. 9.1e-50;  
 Matches 107; Conservative 11; Mismatches 13; Indels 12; Gaps 2;

```

Qy      1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||:||||:|||||||||||||||||| ||||| || | |||||
Db      1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRRENAKNTLYLQMSSLKSEDTALYYC----- 115
        :|||||:| ||| ||| |:|||||||:|:|||||||:|||||||
Db      61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTTV 120

Qy      116 VRYDHYSGSSDYWGQGTTVTVSS 138
        | : ||||| ||||:
Db      121 VPF-----AYWGQGTLLTVSA 136
  
```

RESULT 10

US-08-976-183A-32

```

; Sequence 32, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
  
```

```

Query Match          74.7%; Score 537; Length 136;
Best Local Similarity 74.8%; Pred. No. 1.9e-49;
Matches 107; Conservative 10; Mismatches 14; Indels 12; Gaps 2;

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGFSLIFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
      :| |||||:| ||| ||| |:|||||::|:|||||:|||||
Db      61 EKRLEWVATISSGGSYTYYLDSVKGRFTISRDSARNTLYLQMSSLRSÉDTALYYCAPTTV 120

Qy      116 VRYDHYSGSSDYWGQGTTVTVSS 138
      | : ||||| ||||:
Db      121 VPF-----AYWGQGTTLVTVSA 136

```

```
; Sequence 34, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
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```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-976-183A-34

```

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Query Match          74.5%; Score 536; DB 3; Length 136;
Best Local Similarity 74.1%; Pred. No. 2.4e-49;
Matches 106; Conservative 11; Mismatches 14; Indels 12; Gaps 2;

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Qy      1 MNFGLSLIFLVVLVKGVCQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MNFGFSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
      :|||||:| ||| ||| |:|||||:|:|:|||||:|:|:|||||:|:|:|||||:
Db      61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDALYYCAPTTV 120

Qy      116 VRYDHYSGSSDYWGQGTTVTVSS 138
      | : ||||| ||||:
Db      121 VPF-----AYWGQGTTLVTVA 136

```

```

RESULT 12
US-08-253-877C-57
; Sequence 57, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:

```

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; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-253-877C-57

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```

Query Match          74.4%; Score 535; DB 1; Length 136;
Best Local Similarity 74.1%; Pred. No. 3.1e-49;
Matches 106; Conservative 11; Mismatches 14; Indels 12; Gaps 2;

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Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||:||||:|||||  |||||  |||||  |||||  |||||
Db      1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLSKSEDTALYYC----- 115
        :|||||:| ||| ||| |:|||||:|:|:|||||:|||||
Db     61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSRNTLYLQMSSLRSEDTALYYCAPTTV 120

Qy     116 VRYDHYSGSSDYWGQGTTVTVSS 138
        | : ||||| ||||:
Db     121 VPF-----AYWGQGTTLTVSA 136

```



```

Db          61 EKRLEWVATISSGGSYTTYLLDSVKGRFTISRDSPRNTLYLQMSSLRSEDTALYYCAPTTV 120
Qy          116 VRYDHYSGSSDYWGQGTTVTVSS 138
              | :      ||||| ||||:
Db          121 VPF-----AYWGQGTLLTVTSA 136

```

US-08-053-171-7

; Patent No. 5562903

; TITLE OF INVENTION: Antibody Derivatives

; CORRESPONDENCE ADDRESS:

STREET: 379 Lytton Avenue

; STATE: California

; ZIP: 94301

```

; MEDIUM TYPE: Floppy disk

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```

; COMPUTER: IBM PC compatible

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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
; CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/053,171

; FILING DATE: 22-APR-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Willaim M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-54-1

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 138 amino acids

; TYPE: amino acid

TOPOLOGY: linear

; MOLECULE TYPE: protein

Query Match 74.4%; Score 535; DB 1; Length 138;

Matches 104; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

|   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |     |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|

Qv 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

: ||||| | : || : : | : ||||| : ||||| : ||| : :

RESULT 15

; Sequence 11, Application US/08053171

; Patent No. 5562903

; GENERAL INFORMATION:

; APPLICANT: Co, Loibner

TITLE OF INVENTION: Antibody Derivatives

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

; COUNTRY: US

ZIP: 94301

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,171

; FILING DATE: 22-APR-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Willaim M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-54-1

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-053-171-11

Query Match 74.4%; Score 535; DB 1; Length 138;

Best Local Similarity 75.4%; Pred. No. 3.1e-49;

Matches 104; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Db 1 MNLGLSLIFLVLVLKGVQCEVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTP 60

Db 61 EKRLEWVAYISNGGGSSHYVDSVKGRFTISRDNKNTLYLQMSRLRSEDAMYHCARGMD 120

Qy 121 YSGSSDYWGQTTVTVSS 138  
| | | | | | | | :  
Db 121 YGAWFAYWGQTLVTVSA 138

Search completed: December 13, 2004, 19:19:41  
Job time : 29.6222 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:04:43 ; Search time 24.5333 Seconds  
(without alignments)  
541.219 Million cell updates/sec

Title: US-10-010-942B-4  
Perfect score: 719  
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | % Query |        | DB | ID     | Description             |
|------------|-------|---------|--------|----|--------|-------------------------|
|            |       | Match   | Length |    |        |                         |
| 1          | 573   | 79.7    | 138    | 2  | S09258 | Ig heavy chain V r      |
| 2          | 569   | 79.1    | 152    | 2  | B26471 | Ig heavy chain pre..... |
| 3          | 559.5 | 77.8    | 139    | 2  | S38808 | Ig heavy chain - m      |
| 4          | 544   | 75.7    | 142    | 2  | C34903 | Ig heavy chain pre      |
| 5          | 521.5 | 72.5    | 140    | 2  | S70442 | Ig heavy chain pre      |
| 6          | 517   | 71.9    | 140    | 2  | S31686 | Ig heavy chain V r      |
| 7          | 516   | 71.8    | 160    | 2  | S05271 | Ig heavy chain pre      |
| 8          | 514   | 71.5    | 134    | 2  | S31699 | Ig heavy chain V r      |
| 9          | 513   | 71.3    | 140    | 2  | S31588 | Ig heavy chain V r      |
| 10         | 512   | 71.2    | 117    | 1  | HVMS84 | Ig heavy chain pre      |
| 11         | 510   | 70.9    | 117    | 1  | HVMS34 | Ig heavy chain pre      |
| 12         | 508   | 70.7    | 136    | 2  | S31615 | hypothetical prote      |
| 13         | 504   | 70.1    | 140    | 2  | S22657 | Ig heavy chain pre      |

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 14 | 502.5 | 69.9 | 136 | 1 | G1MS21 | Ig heavy chain pre |
| 15 | 502   | 69.8 | 138 | 2 | S31666 | Ig heavy chain V r |
| 16 | 501   | 69.7 | 117 | 1 | HVMS39 | Ig heavy chain pre |
| 17 | 495   | 68.8 | 135 | 2 | S31598 | Ig heavy chain V r |
| 18 | 493   | 68.6 | 134 | 2 | S31679 | Ig heavy chain V r |
| 19 | 492.5 | 68.5 | 141 | 2 | S31669 | Ig heavy chain V r |
| 20 | 492   | 68.4 | 117 | 1 | HVMSRF | Ig heavy chain pre |
| 21 | 492   | 68.4 | 139 | 2 | I37781 | Ig variable region |
| 22 | 490   | 68.2 | 122 | 2 | E27888 | Ig heavy chain V r |
| 23 | 487.5 | 67.8 | 119 | 2 | F27888 | Ig heavy chain V r |
| 24 | 485.5 | 67.5 | 136 | 2 | S31587 | Ig heavy chain V r |
| 25 | 484.5 | 67.4 | 151 | 2 | A60943 | Ig heavy chain pre |
| 26 | 484   | 67.3 | 117 | 1 | HVMS57 | Ig heavy chain pre |
| 27 | 484   | 67.3 | 140 | 2 | A30532 | Ig heavy chain pre |
| 28 | 483   | 67.2 | 120 | 2 | S55536 | Ig heavy chain V r |
| 29 | 481.5 | 67.0 | 147 | 2 | I37780 | Ig variable region |
| 30 | 480.5 | 66.8 | 118 | 2 | PH0096 | Ig heavy chain V r |
| 31 | 480.5 | 66.8 | 121 | 2 | S55540 | Ig heavy chain V r |
| 32 | 480.5 | 66.8 | 254 | 2 | B31790 | Ig heavy chain V r |
| 33 | 479   | 66.6 | 120 | 2 | S55538 | Ig heavy chain V r |
| 34 | 479   | 66.6 | 120 | 2 | S55539 | Ig heavy chain V r |
| 35 | 477.5 | 66.4 | 121 | 2 | H27888 | Ig heavy chain V r |
| 36 | 477.5 | 66.4 | 137 | 2 | S31701 | Ig heavy chain V r |
| 37 | 477.5 | 66.4 | 139 | 2 | S31674 | Ig heavy chain V r |
| 38 | 476.5 | 66.3 | 137 | 2 | S78054 | Ig heavy chain pre |
| 39 | 476   | 66.2 | 120 | 2 | S55537 | Ig heavy chain V r |
| 40 | 473.5 | 65.9 | 118 | 2 | PH0097 | Ig heavy chain V r |
| 41 | 472   | 65.6 | 132 | 2 | S31603 | Ig heavy chain V r |
| 42 | 471   | 65.5 | 130 | 2 | PL0098 | Ig heavy chain pre |
| 43 | 469   | 65.2 | 118 | 2 | S20641 | Ig heavy chain V r |
| 44 | 467.5 | 65.0 | 135 | 2 | I37778 | Ig variable region |
| 45 | 467.5 | 65.0 | 145 | 2 | S11239 | Ig heavy chain V r |

#### ALIGNMENTS

##### RESULT 1

S09258

Ig heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 23-Jul-1999

C;Accession: S09258

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK16.

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09258

A;Molecule type: DNA

A;Residues: 1-138 <HAM>

A;Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 573; DB 2; Length 138;  
Best Local Similarity 80.4%; Pred. No. 5.8e-43;  
Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||:||||| ||||| |||||:| |||||
Db      1 MNFGLSLIFLVLILKGVQCEVILVESGGGLVKPGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          :|||||:| ||| ||| |:|||||:|||| |||||:||||| ||
Db     61 EKRLEWVATISSGGGNTYYPDSVKGRFTISRDNANKNNLYLQMSSLRSEDTALYYCARYYR 120

Qy    121 YSGSSDYWGQGTTVTVSS 138
          | |||| |||:
Db    121 YEAWFASWGQGTTLTVSA 138
```

## RESULT 2

B26471

Ig heavy chain precursor V region (MAK33) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999

C;Accession: B26471; S70410

R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.  
Gene 51, 13-19, 1987

A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a  
creatine-kinase-specific monoclonal antibody.

A;Reference number: A91572; MUID:87248058; PMID:3110009

A;Accession: B26471

A;Molecule type: mRNA

A;Residues: 1-152 <BUC>

A;Cross-references: GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:g195406

R;Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 172, 1717-1727, 1990

A;Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5'  
boundary is near the promoter, and 3' boundary is about 1 kb from V(D)J gene.

A;Reference number: S70410; MUID:91079775; PMID:2258702

A;Accession: S70410

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-19 <LEB>

A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 569; DB 2; Length 152;  
Best Local Similarity 78.2%; Pred. No. 1.4e-42;  
Matches 111; Conservative 10; Mismatches 17; Indels 4; Gaps 1;

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Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||:||||| ||||| |||||:| |||||
```

```

Db          1 MNFGLSLIFLVLVLKGVQCEVQGVESGGGLVKPGGSLKLSCAASGFTFSDDYYMYWVRQTP 60
Qy          61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
              :|||||||:| || ||| |:|||||||:|||| |||||||||:|||| |
Db          61 EKRLEWVATISDGGSYTYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYCARDKA 120

Qy          118 -YDHYSGSSDYWGQGTTVTVSS 138
              | :| : |||||||:|||||
Db          121 YYGNYGDAMDYWGQGTSTVTVSS 142

```

### RESULT 3

S38808

Ig heavy chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000

C;Accession: S38808

R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.

Immunogenetics 36, 15-21, 1992

A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2b antibody with rheumatoid factor activity.

A;Reference number: S38807; MUID:92267566; PMID:1587549

A;Accession: S38808

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <SEQ>

A;Cross-references: EMBL:X53400

A;Note: the authors translated the codon GAG for residue 117 as Lys

A;Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are not shown in this paper

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-116/Domain: immunoglobulin homology <IMM>

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Query Match          77.8%; Score 559.5; DB 2; Length 139;
Best Local Similarity 79.3%; Pred. No. 8.7e-42;
Matches 111; Conservative 8; Mismatches 16; Indels 5; Gaps 2;

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Qy          1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
              |||| |||||||||||||||||||||||||||| |||||||||:| |||||
Db          1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFTFSYAMS WVRQTP 60

Qy          61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
              :||||||| | || ||| |:|||||||:|:| |||||||:||||:| |
Db          61 EKRLEWVASI-SRGGTTYYPDSVKGRFTISRDNARNNLYLQMSSLRSEDTAMYCAREGI 119

Qy          121 YSG----SSDYWGQGTTVTV 136
              | | |||||||:| |
Db          120 YGYALYGM DYWGQGTSTVTV 139

```

### RESULT 4

C34903

Ig heavy chain precursor V region (5-27) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996

C;Accession: C34903

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

F;34-119/Domain: immunoglobulin homology <IMM>

F;34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Qv 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLOMSSLKSEDTALYYCVRYDH 120



A;Cross-references: UNIPROT:Q96BB9; EMBL:X14584  
 R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.  
 Nucleic Acids Res. 17, 4385, 1989  
 A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells.  
 A;Reference number: S04601; MUID:89296497; PMID:2500644  
 A;Accession: S04602  
 A;Molecule type: mRNA  
 A;Residues: 1-144 <KIS2>  
 A;Cross-references: EMBL:X14584  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>  
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 516; DB 2; Length 160;  
 Best Local Similarity 68.1%; Pred. No. 6.2e-38;  
 Matches 98; Conservative 18; Mismatches 22; Indels 6; Gaps 1;

```
Qy      1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | | | | : | | : | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
      | | | | : : | | | | : | | | | | | | | | | | | | | | | | :
Db     61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAVV 120

Qy    118 ---YDHYSGSSDYWGQGTTTVTVSS 138
      : | | | | | | | | |
Db    121 RGVISYYYYGMDVWGQGTTTVTVSS 144
```

# RESULT 8

S31699

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S31699

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31699

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-134 <CUI>

A;Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 514; DB 2; Length 134;  
 Best Local Similarity 71.0%; Pred. No. 7.7e-38;  
 Matches 98; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | | | | : | | : | | | | | | : | | | | | | | | | | | | | | | |
Db      1 MEFGLSWLFLVAILKGVQCEVQLLES GGGLVHPGGSRLRLSCAASGFTFSSYAMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 GKGLEWVSAISGSGGSTYYSDSVKGRLTISRDN SKNTLYLQMNSLRAEDTAVYYCARW-- 118

Qy      121 YSGSSDYWGQGT TVTVSS 138
      | | | | | | | | | |
Db      119 --RDL DYWGQGT LVTVSS 134

```

# RESULT 9

S31588

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S31588

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate  
from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31588

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

```

Query Match          71.3%;  Score 513;  DB 2;  Length 140;
Best Local Similarity 69.3%;  Pred. No. 9.8e-38;
Matches 97;  Conservative 20;  Mismatches 21;  Indels 2;  Gaps 1;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | | | | : | | : | | | | | | : | | | | | | | | | | | | | | | |
Db      1 MEFGLSWLFLVAILRGVQCEVQLLES GGGLVQPGGSRLRLSCAASGFTFSSYAMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYYCAKDHD 120

Qy      121 YSG--SSDYWGQGT TVTVSS 138
      | | | | | | | | | |
Db      121 YSNYIYFDYWGQGT LVTVSS 140

```

# RESULT 10

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004

C;Accession: JT0505

R;Levy, N.S.; Maliplero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the  
primary immune response.  
A;Reference number: JT0501; MUID:89279149; PMID:2499654  
A;Accession: JT0505  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-117 <LEV>  
A;Cross-references: UNIPROT:P18525  
A;Experimental source: strain BALB/cJ  
A;Note: this sequence belongs to the VH7183 subfamily  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>  
F;41-115/Disulfide bonds: #status predicted

RESULT 11

Ig heavy chain precursor V region (345) - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
 C;Accession: JT0502  
 R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
 J. Exp. Med. 169, 2007-2019, 1989  
 A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the  
 primary immune response.  
 A;Reference number: JT0501; MUID:89279149; PMID:2499654  
 A;Accession: JT0502  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-117 <LEV>  
 A;Cross-references: UNIPROT:P18526  
 A;Experimental source: strain BALB/cJ  
 A;Note: this sequence belongs to the VH7183 subfamily  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>  
 F;34-117/Domain: immunoglobulin homology <IMM>  
 F;41-115/Disulfide bonds: #status predicted

Query Match 70.9%; Score 510; DB 1; Length 117;  
 Best Local Similarity 83.8%; Pred. No. 1.5e-37;  
 Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 ||||| ||||| ||||:||||:||||||| ||||| ||:| |||||  
 Db 1 MNFGLRLIFLVLTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60  
 Qy 61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117  
 :||||||| | |||| ||| | |||||:|||||||:|||||  
 Db 61 EKRLEWVAYISSGGGSTYYPDTPVKGRFTISRDNKNTLYLQMSSLKSEDTAMYYCAR 117

# RESULT 12

S31615

hypothetical protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S31615

R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, April 1991

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for antidioxin monoclonal.

A;Reference number: S31615

A;Accession: S31615

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <REC>

A;Cross-references: EMBL:X58884; NID:g51824; PIDN:CAA41688.1; PID:g51825

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 508; DB 2; Length 136;  
 Best Local Similarity 70.3%; Pred. No. 2.6e-37;  
 Matches 97; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 ||||| ||||| ||||:| |||||:|||||:||||| || | |||||  
 Db 1 MNFGLRLIFLVLTLKGVQCDVNLVESGGGLVKPGGTLKLSCSASGFAFSTYSMVWVRQTP 60  
 Qy 61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120  
 :||||||:| || ||| |:|:|||||:|:| || |:|:|||||:|:| |  
 Db 61 EKRLEWVATITGGGTYTYYPDSVRGRFTISRDNARDTLNLHMTNLKSEDTAMYYCLGYW 120  
 Qy 121 YSGSSDYWGQGTTVTVSS 138  
 | |: ||||| | ||:  
 Db 121 YDGT--YWGQGTIVIVSA 136

# RESULT 13

S22657

Ig heavy chain precursor V region (0-81VH) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 06-Feb-1998

C;Accession: S22657

R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.

A;Reference number: S22657; MUID:92285150; PMID:1598223

A;Accession: S22657

A;Molecule type: mRNA

A;Residues: 1-140 <HIR>

A;Cross-references: EMBL:X59134

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-140/Product: Ig heavy chain (fragment) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 504; DB 2; Length 140;

Best Local Similarity 68.1%; Pred. No. 6e-37;

Matches 94; Conservative 21; Mismatches 19; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVQPGASLKLSCAASGFTFSNYGMSWVRQNS 60

| |||| :||| :||| ||||| :||||||| :|| ||:||||||| :||| :|||

Db 1 MEFGLSWVFLVAILEGVQCEVQLVESGGGLVQPGSLRLSCAASGFTFSSHWMTWVRQTP 60

Qy 61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKSSEDALYYCVRYDH 120

||||| :||| | ||:|:|:||||| :|||:|||| | :||:|:| |

Db 61 GKRLEWVANVKQDGSARYYADSVRGRFTISRDNAKNSLYLQMSLRLADDTAVYYCAR--- 117

Qy 121 YGSSDYWGQGTTLTVSS 138

| ||||| |||||

Db 118 -STGIDYWGQGTTLTVSS 134

#### RESULT 14

GLMS21

Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004

C;Accession: E90809; A93184; A02066

R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.

Cell 24, 625-637, 1981

A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: somatic mutation evident in a gamma2a variable region.

A;Reference number: A90809; MUID:81234548; PMID:6788376

A;Accession: E90809

A;Molecule type: mRNA

A;Residues: 1-136 <BOT>

A;Cross-references: UNIPROT:P01783; GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055

R;Adetugbo, K.; Milstein, C.; Secher, D.S.

Nature 265, 299-304, 1977

A;Title: Molecular analysis of spontaneous somatic mutants.

A;Reference number: A93184; MUID:77100368; PMID:401950

A;Contents: myeloma protein MOPC 21

A;Accession: A93184

A;Molecule type: protein

A;Residues: 17-74,'D',76-77,'H',79-88,'ND',91-114,'H',116-119,'W',121-136 <ADE>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin



| :: | ||:| | |||  
Db 121 GYWYF----DLWGRGTLVTVSS 138

Search completed: December 13, 2004, 19:18:39  
Job time : 24.5333 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:17:53 ; Search time 99.1556 Seconds  
(without alignments)  
497.104 Million cell updates/sec

Title: US-10-010-942B-4  
Perfect score: 719  
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result | Query |       |        |    |                   | Description       |
|--------|-------|-------|--------|----|-------------------|-------------------|
| No.    | Score | Match | Length | DB | ID                |                   |
| 1      | 719   | 100.0 | 138    | 14 | US-10-010-942B-4  | Sequence 4, Appli |
| 2      | 719   | 100.0 | 138    | 15 | US-10-388-389-4   | Sequence 4, Appli |
| 3      | 719   | 100.0 | 138    | 16 | US-10-703-713-4   | Sequence 4, Appli |
| 4      | 719   | 100.0 | 138    | 16 | US-10-704-070-4   | Sequence 4, Appli |
| 5      | 652   | 90.7  | 138    | 14 | US-10-010-942B-8  | Sequence 8, Appli |
| 6      | 652   | 90.7  | 138    | 15 | US-10-388-389-8   | Sequence 8, Appli |
| 7      | 652   | 90.7  | 138    | 16 | US-10-703-713-8   | Sequence 8, Appli |
| 8      | 652   | 90.7  | 138    | 16 | US-10-704-070-8   | Sequence 8, Appli |
| 9      | 650   | 90.4  | 138    | 14 | US-10-010-942B-12 | Sequence 12, Appl |
| 10     | 650   | 90.4  | 138    | 15 | US-10-388-389-12  | Sequence 12, Appl |
| 11     | 650   | 90.4  | 138    | 16 | US-10-703-713-12  | Sequence 12, Appl |
| 12     | 650   | 90.4  | 138    | 16 | US-10-704-070-12  | Sequence 12, Appl |
| 13     | 609.5 | 84.8  | 133    | 13 | US-10-006-773-9   | Sequence 9, Appli |
| 14     | 578.5 | 80.5  | 139    | 13 | US-10-006-773-17  | Sequence 17, Appl |
| 15     | 578   | 80.4  | 462    | 14 | US-10-281-479A-23 | Sequence 23, Appl |
| 16     | 578   | 80.4  | 462    | 14 | US-10-286-132A-23 | Sequence 23, Appl |
| 17     | 578   | 80.4  | 464    | 14 | US-10-275-180A-23 | Sequence 23, Appl |
| 18     | 569   | 79.1  | 144    | 9  | US-09-881-823-12  | Sequence 12, Appl |
| 19     | 566   | 78.7  | 140    | 9  | US-09-286-240-4   | Sequence 4, Appli |
| 20     | 559   | 77.7  | 140    | 13 | US-10-006-773-4   | Sequence 4, Appli |
| 21     | 557.5 | 77.5  | 137    | 9  | US-09-423-800-76  | Sequence 76, Appl |
| 22     | 557.5 | 77.5  | 137    | 14 | US-10-337-981-76  | Sequence 76, Appl |
| 23     | 553   | 76.9  | 158    | 15 | US-10-226-795-32  | Sequence 32, Appl |
| 24     | 549   | 76.4  | 140    | 14 | US-10-283-349-23  | Sequence 23, Appl |
| 25     | 542   | 75.4  | 140    | 15 | US-10-365-123-51  | Sequence 51, Appl |
| 26     | 537   | 74.7  | 159    | 14 | US-10-291-265-333 | Sequence 333, App |
| 27     | 531.5 | 73.9  | 143    | 10 | US-09-791-551-117 | Sequence 117, App |
| 28     | 528   | 73.4  | 143    | 15 | US-10-469-304-17  | Sequence 17, Appl |
| 29     | 526.5 | 73.2  | 177    | 16 | US-10-693-629-64  | Sequence 64, Appl |
| 30     | 522   | 72.6  | 313    | 14 | US-10-291-265-427 | Sequence 427, App |
| 31     | 522   | 72.6  | 470    | 15 | US-10-038-591-46  | Sequence 46, Appl |
| 32     | 522   | 72.6  | 470    | 17 | US-10-775-444A-46 | Sequence 46, Appl |
| 33     | 520.5 | 72.4  | 469    | 14 | US-10-292-088-54  | Sequence 54, Appl |
| 34     | 514.5 | 71.6  | 139    | 10 | US-09-947-839-96  | Sequence 96, Appl |
| 35     | 514.5 | 71.6  | 139    | 17 | US-10-478-056-33  | Sequence 33, Appl |
| 36     | 514   | 71.5  | 138    | 9  | US-09-796-744-15  | Sequence 15, Appl |
| 37     | 514   | 71.5  | 138    | 14 | US-10-231-452-62  | Sequence 62, Appl |
| 38     | 512   | 71.2  | 465    | 14 | US-10-401-344-2   | Sequence 2, Appli |
| 39     | 510.5 | 71.0  | 137    | 9  | US-09-423-800-77  | Sequence 77, Appl |
| 40     | 510.5 | 71.0  | 137    | 14 | US-10-337-981-77  | Sequence 77, Appl |
| 41     | 510.5 | 71.0  | 473    | 15 | US-10-038-591-50  | Sequence 50, Appl |
| 42     | 510.5 | 71.0  | 473    | 17 | US-10-775-444A-50 | Sequence 50, Appl |
| 43     | 508.5 | 70.7  | 307    | 14 | US-10-291-265-332 | Sequence 332, App |
| 44     | 508.5 | 70.7  | 363    | 14 | US-10-291-265-335 | Sequence 335, App |
| 45     | 506   | 70.4  | 474    | 10 | US-09-848-832-3   | Sequence 3, Appli |

#### ALIGNMENTS

##### RESULT 1

US-10-010-942B-4

; Sequence 4, Application US/10010942B

; Publication No. US20030165496A1.

```
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-4
```

```
Query Match          100.0%; Score 719; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.6e-60;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVVLVKGVCQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||
Db      1 MNFGLSLIFLVVLVKGVCQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

Qy     61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          |||
Db     61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

Qy     121 YSGSSDYWGQGTTVTVSS 138
          |||
Db     121 YSGSSDYWGQGTTVTVSS 138
```

#### RESULT 2

US-10-388-389-4

```
; Sequence 4, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
```



Query Match 100.0%; Score 719; DB 16; Length 138;  
Best Local Similarity 100.0%; Pred. No. 6.6e-60;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS | 60  |
|    |     |  |     |
| Db | 1   | MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS | 60  |
| Qy | 61  | DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH | 120 |
|    |     |  |     |
| Db | 61  | DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH | 120 |
| Qy | 121 | YSGSSDYWGQGTTVTVSS   | 138 |
|    |     |  |     |
| Db | 121 | YSGSSDYWGQGTTVTVSS   | 138 |

#### RESULT 4

US-10-704-070-4

; Sequence 4, Application US/10704070

; Publication No. US20040171816A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig

; APPLICANT: Saldanha, Jose

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

; FILE REFERENCE: ELN-002CP

; CURRENT APPLICATION NUMBER: US/10/704,070

; CURRENT FILING DATE: 2003-11-07

; PRIOR APPLICATION NUMBER: 10/388,389

; PRIOR FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US 10/010,942

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: US 60/251,892

; PRIOR FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 63

```
; SOFTWARE: FastSEQ for Windows Version 4.0
```

; SEQ ID NO 4

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Mus musculus

FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)...(19)

US-10-704-070-4

Query Match 100.0%; Score 719; DB 16; Length 138;  
Best Local Similarity 100.0%; Pred. No. 6.6e-60;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |    |  |     |
|----|----|--|-----|
| Qy | 1  | MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS | 60  |
|    |    |  |     |
| Db | 1  | MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS | 60  |
|    |    |  |     |
| Qy | 61 | DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH | 120 |
|    |    |  |     |





```
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-703-713-8
```

```
Query Match          90.7%; Score 652; DB 16; Length 138;
Best Local Similarity 89.1%; Pred. No. 1.3e-53;
Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||:|||||:|:|||||:|:|:|||||:|||||
Db      1 MNFGLSLIFLVLVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRDNKNTLYLQMSLKSSEDALYYCVRYDH 120
          | |||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNKNTLYLQMSLRAEDTALYYCVRYDH 120

Qy      121 YSGSSDYWGQGTTLTVTVSS 138
          |||:|||||:|:|
Db      121 YSGSSDYWGQGTTLTVTVSS 138
```

# RESULT 8

US-10-704-070-8

```
; Sequence 8, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-704-070-8
```

Query Match 90.7%; Score 652; DB 16; Length 138;  
Best Local Similarity 89.1%; Pred. No. 1.3e-53;  
Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

|      |  |   |     |
|------|--|---|-----|
| Qy   |  | 1 MNFGLSLIFLVLVLRKGVQCSEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSSWVRONS   | 60  |
|      |  | :   :         :       :   |     |
| Db   |  | 1 MNFGLSLIFLVLVLRKGVQCSEVQLLESGGGLVQPGGSLRLSCLAAAGFTFSNYGMSSWVRQAAP | 60  |
| <br> |  |   |     |
| Qy   |  | 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNLTLYLQMSSLKSSEDALYVCVRYDH    | 120 |
|      |  | :     :       :   :   |     |
| Db   |  | 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNAKNSLYLQMNSLRAEDTALYVCVRYDH     | 120 |
| <br> |  |   |     |
| Qy   |  | 121 YSGSSDYWGQGTTVTVSS  | 138 |
|      |  |   |     |
| Db   |  | 121 YSGSSDYWGQGTTLTVSS  | 138 |

## RESULT 9

US-10-010-942B-12

; Sequence 12, Application US/10010942B

; Publication No. US20030165496A1

## ; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig

APPLICANT: Saldanha, Jose

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

; TITLE OF INVENTION: BETA AMYLOID PEPTIDE

; FILE REFERENCE: ELN-002

; CURRENT APPLICATION NUMBER: US/10/010,942B

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: US 60/251,892

; PRIOR FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 63

```
; SOFTWARE: FastSEQ for Windows Version 4.0
```

; SEQ ID NO 12

; LENGTH: 138

; TYPE: PRT

```
; ORGANISM: Artificial Sequence
```

; FEATURE:

; OTHER INFORMATION: Humanized 3D6 light chain variable region

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1) ... (19)

US-10-010-942B-12

Query Match 90.4%; Score 650; DB 14; Length 138;  
Best Local Similarity 88.4%; Pred. No. 2.1e-53;  
Matches 122; Conservative 10; Mismatches 6; Indels 0; Gaps 0;



Db                    |||||     |||||  
121 YSGSSDYWGQGT LVT VSS 138

RESULT 11

US-10-703-713-12

; Sequence 12, Application US/10703713  
; Publication No. US20040171815A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Guriq  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/703,713  
; CURRENT FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized 3D6 light chain variable region  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(19)  
US-10-703-713-12

Query Match                    90.4%;    Score 650;    DB 16;    Length 138;  
Best Local Similarity    88.4%;    Pred. No. 2.1e-53;  
Matches 122;    Conservative    10;    Mismatches    6;    Indels    0;    Gaps    0;

Qy                    1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
                      |||||     |||||     |||||     |||||     |||||     |||||     |||||     |||||     |||||  
Db                    1 MNFGLSLIFLVLVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60  
  
Qy                    61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRDNKNTLYLQMSLKS EDTALYYCVRYDH 120  
                      | |||||     |||||     |||||     |||||     |||||     |||||     |||||     |||||     |||||  
Db                    61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCVRYDH 120  
  
Qy                    121 YSGSSDYWGQGT TTVTVSS 138  
                      |||||     |||||  
Db                    121 YSGSSDYWGQGT LVT VSS 138

RESULT 12

US-10-704-070-12

; Sequence 12, Application US/10704070  
; Publication No. US20040171816A1



; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-9

Query Match 84.8%; Score 609.5; DB 13; Length 133;  
Best Local Similarity 87.0%; Pred. No. 1.3e-49;  
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||:|||||
Db      1 MNFGLSLIFLVVLKGVQCEVKVVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVRYDH 120
          |||:|||||
Db      61 DKRLEWVASISSGGDSTFYADNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCARDL 120

Qy      121 YSGSSDYWGQGT TVTVSS 138
          :: |||||
Db      121 FN-----WGQGT TLTVSS 133
```

#### RESULT 14

US-10-006-773-17

; Sequence 17, Application US/10006773  
; Publication No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Junghans, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against  
Tumor Antigens  
; FILE REFERENCE: 003  
; CURRENT APPLICATION NUMBER: US/10/006,773  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250,089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-17

Query Match 80.5%; Score 578.5; DB 13; Length 139;  
Best Local Similarity 82.7%; Pred. No. 1.1e-46;  
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||:|||||
Db      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLMNP GASLKLSCAASGFSFSNYGMSWVRQTS 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVRYDH 120
          |||:|||||
```



Qy 121 YSGSSDYWGQGTTVTVSS 138  
::|||||||:||||  
Db 121 SMITTDYWGQGTTLTVSS 138

Search completed: December 13, 2004, 19:34:50  
Job time : 100.156 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2004, 18:50:06 ; Search time 131.356 Seconds  
(without alignments)  
604.479 Million cell updates/sec

Title: US-10-010-942B-4  
Perfect score: 719  
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID         | Description        |
|------------|-------|---------|--------------|----|------------|--------------------|
| 1          | 576.5 | 80.2    | 487          | 2  | Q99KA4     | Q99ka4 mus musculu |
| 2          | 557   | 77.5    | 479          | 2  | Q91WP5     | Q91wp5 mus musculu |
| 3          | 547   | 76.1    | 486          | 2  | Q91Z07     | Q91z07 mus musculu |
| 4          | 529   | 73.6    | 485          | 2  | Q6PDB8     | Q6pdb8 mus musculu |
| 5          | 529   | 73.6    | 485          | 2  | AAH58814   | Aah58814 mus muscu |
| 6          | 516.5 | 71.8    | 473          | 2  | Q91Z05     | Q91z05 mus musculu |
| 7          | 512   | 71.2    | 117          | 1  | HV54_MOUSE | P18525 mus musculu |
| 8          | 510   | 70.9    | 117          | 1  | HV55_MOUSE | P18526 mus musculu |
| 9          | 505   | 70.2    | 480          | 2  | Q91XE1     | Q91xe1 mus musculu |
| 10         | 503   | 70.0    | 597          | 2  | Q96BB9     | Q96bb9 homo sapien |
| 11         | 502.5 | 69.9    | 136          | 1  | HV16_MOUSE | P01783 mus musculu |
| 12         | 501   | 69.7    | 117          | 1  | HV59_MOUSE | P18530 mus musculu |
| 13         | 499   | 69.4    | 478          | 2  | Q6PI81     | Q6pi81 homo sapien |
| 14         | 499   | 69.4    | 478          | 2  | AAH41037   | Aah41037 homo sapi |
| 15         | 495.5 | 68.9    | 606          | 2  | Q6GMY2     | Q6gmy2 homo sapien |

|    |       |      |     |   |            |                    |
|----|-------|------|-----|---|------------|--------------------|
| 16 | 492   | 68.4 | 117 | 1 | HV53_MOUSE | P18524 mus musculu |
| 17 | 492   | 68.4 | 119 | 2 | Q920E7     | Q920e7 mus musculu |
| 18 | 490   | 68.2 | 255 | 2 | Q6KB05     | Q6kb05 mus musculu |
| 19 | 490   | 68.2 | 255 | 2 | CAG34081   | Cag34081 mus muscu |
| 20 | 490   | 68.2 | 499 | 2 | Q8N5K4     | Q8n5k4 homo sapien |
| 21 | 487   | 67.7 | 464 | 2 | Q6MZU6     | Q6mzu6 homo sapien |
| 22 | 487   | 67.7 | 464 | 2 | CAE45931   | Cae45931 homo sapi |
| 23 | 486.5 | 67.7 | 613 | 2 | Q8WUK1     | Q8wuk1 homo sapien |
| 24 | 486   | 67.6 | 470 | 2 | Q6PJA4     | Q6pja4 homo sapien |
| 25 | 486   | 67.6 | 470 | 2 | AAH18747   | Aah18747 homo sapi |
| 26 | 484   | 67.3 | 117 | 1 | HV58_MOUSE | P18529 mus musculu |
| 27 | 483.5 | 67.2 | 573 | 2 | Q8WU38     | Q8wu38 homo sapien |
| 28 | 477.5 | 66.4 | 471 | 2 | AAH24289   | Aah24289 homo sapi |
| 29 | 475   | 66.1 | 472 | 2 | Q6N089     | Q6n089 homo sapien |
| 30 | 475   | 66.1 | 472 | 2 | CAE45781   | Cae45781 homo sapi |
| 31 | 473   | 65.8 | 493 | 2 | Q6GMX2     | Q6gm2 homo sapien  |
| 32 | 471   | 65.5 | 493 | 2 | Q8NCL6     | Q8ncl6 homo sapien |
| 33 | 468.5 | 65.2 | 475 | 2 | Q6MZQ6     | Q6mzq6 homo sapien |
| 34 | 468.5 | 65.2 | 475 | 2 | CAE45972   | Cae45972 homo sapi |
| 35 | 464   | 64.5 | 128 | 2 | BAD00406   | Bad00406 camelus d |
| 36 | 464   | 64.5 | 464 | 2 | BAC85395   | Bac85395 homo sapi |
| 37 | 463.5 | 64.5 | 465 | 2 | Q6P6C4     | Q6p6c4 homo sapien |
| 38 | 463.5 | 64.5 | 465 | 2 | AAH62335   | Aah62335 homo sapi |
| 39 | 463   | 64.4 | 117 | 1 | HV3C_HUMAN | P01764 homo sapien |
| 40 | 463   | 64.4 | 117 | 2 | AAL35877   | Aal35877 lama glam |
| 41 | 462.5 | 64.3 | 479 | 2 | AAH06402   | Aah06402 homo sapi |
| 42 | 461.5 | 64.2 | 494 | 2 | Q96K68     | Q96k68 homo sapien |
| 43 | 460.5 | 64.0 | 473 | 2 | Q6MZV7     | Q6mzv7 homo sapien |
| 44 | 460.5 | 64.0 | 473 | 2 | CAE45920   | Cae45920 homo sapi |
| 45 | 460   | 64.0 | 497 | 2 | BAC86210   | Bac86210 homo sapi |

# ALIGNMENTS

## RESULT 1

Q99KA4

ID Q99KA4 PRELIMINARY; PRT; 487 AA.

AC Q99KA4;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE LOC380791 protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Czech II;

RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Czech II;  
 RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC004786; AAH04786.1; -.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 80.2%; Score 576.5; DB 2; Length 487;  
 Best Local Similarity 79.2%; Pred. No. 4.6e-49;  
 Matches 114; Conservative 7; Mismatches 16; Indels 7; Gaps 2;

QY 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |||||||||||||||||||:||||||||| |||||||||||||:| |||||  
 Db 1 MNFGLSLIFLVLVLKGVQCEVLVESGGGLVKPGSLKLSCAASGFTFSSYAMSWVRQTP 60  
 QY 61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117  
 :|||||||:| || ||| |||||||||||:|||| ||||| |||||||:||| |  
 Db 61 EKRLEWVATISDGGSYTYYPDNVKGRTISRDNAKNNLYLQMSHLKSEDTAMYCARDMG 120  
 QY 118 ---YDHYSGSSDYWGQGTTVTVSS 138  
 | || |||||||:||||  
 Db 121 GSPYGGYS-RFDYWQGTITVSS 143

## RESULT 2

Q91WP5

ID Q91WP5 PRELIMINARY; PRT; 479 AA.  
 AC Q91WP5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Igh-VJ558 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC013656; AAH13656.1; -.  
 DR HSSP; P01789; 1MCP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 77.5%; Score 557; DB 2; Length 479;  
 Best Local Similarity 78.3%; Pred. No. 4e-47;  
 Matches 108; Conservative 10; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||  
 Db 1 MNFGLTLIFLVLTLKGVQCEVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSP 60  
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKSSEDALYYCVRYDH 120

```

          :|||||||:| | || ||||| :|||||||:||||:|||||||:||||| |||||
Db          61 EKRLEWVAAINSNGGNTYYSDTMKGRFTISRDNASTLYLQMSSLRSEDTAIFYCVR--- 117

QY          121 YSGSSDYWGQGTTVTVSS 138
          | | || || |||||
Db          118 -GGYFDVWGAGTAVTVSS 134

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RESULT 3

Q91Z07

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ID   Q91Z07          PRELIMINARY;          PRT;          486 AA.
AC   Q91Z07;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   LOC380791 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010324; AAH10324.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.

```

DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 486 AA; 52681 MW; 4FEF835125DA870B CRC64;

Query Match 76.1%; Score 547; DB 2; Length 486;  
 Best Local Similarity 76.2%; Pred. No. 4.1e-46;  
 Matches 109; Conservative 12; Mismatches 16; Indels 6; Gaps 3;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1 MNFGLRLIFLVLALKGVQCEVHLVESGGGLVKPGGSLKLSKLVVSGFSFTSYDMSWVRQTP 60  
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKSEDTALYYCVRVD- 119  
 ::|||::| | | | | |||||::||:| | ||||| ||||| ||||| ||||| :  
 Db 61 ERRLEWVAITS-GGNTYYPDNVKGRTVSRDNAKYTLYLQMSLKSEDTAMYYCVRPEI 119  
 Qy 120 ---HYSGS-SDYWGGTTTVTVSS 138  
 :||| | |||||:||||  
 Db 120 PIYYYSYFDSWGQTTITVSS 142

#### RESULT 4

##### Q6PDB8

ID Q6PDB8 PRELIMINARY; PRT; 485 AA.  
 AC Q6PDB8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC058814; AAH58814.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.....  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00407; IGc1; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 485 AA; 52472 MW; 81236FF3AD821056 CRC64;

Query Match 73.6%; Score 529; DB 2; Length 485;  
 Best Local Similarity 71.4%; Pred. No. 2.6e-44;  
 Matches 100; Conservative 17; Mismatches 21; Indels 2; Gaps 1;

QY 1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |: :|:||||:|||||:|:||||||| || | ||||| ||||| |||||  
 Db 1 MDSRFNLVFLVLILKGVQCDVQLVESGGGLVPPGGSRLKSCAASGFTFSNYGMHWVRQAP 60  
 QY 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--Y 118  
 :| ||||| | | | :|:| |||||:|||||:|:|:|:|:|:| | | |  
 Db 61 EGGLEWVAYISSSSGTIFYADTVKGRFTISRDNKNTLFLQMTSLRSEDATAMYYCARLYY 120  
 QY 119 DHYSGSSDYWGQGTTVTVSS 138  
 :| |: |||||:|||||  
 Db 121 SNYGGAMDYWGQGTSVTVSS 140

# RESULT 5 AAH58814

ID AAH58814 PRELIMINARY; PRT; 485 AA.....  
 AC AAH58814;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC058814; AAH58814.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 485 AA; 52472 MW; 81236FF3AD821056 CRC64;

Query Match 73.6%; Score 529; DB 2; Length 485;  
 Best Local Similarity 71.4%; Pred. No. 2.6e-44;  
 Matches 100; Conservative 17; Mismatches 21; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 |: :|:||||:|||||:|:||||||| || | ||||||||| |||||  
 Db 1 MDSRFNLVFLVLILKGVQCDVQLVESGGGLVPPGGSRLKSCAASGFTFSNYGMHWVRQAP 60  
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--Y 118  
 :| ||||| | | | :|:| |||||||:|||||:|:|:|:|:|:| | |  
 Db 61 EGGLEWVAYISSSSGTIFYADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARLYY 120  
 Qy 119 DHYSGSSDYWGQGTTVTVSS 138  
 :| |: ||||||:|||||  
 Db 121 SNYGGAMDYWGQTSVTVSS 140

RESULT 6  
 Q91Z05

ID Q91Z05 PRELIMINARY; PRT; 473 AA.  
 AC Q91Z05;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Expressed sequence AU044919.  
 GN Name=AU044919;

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer.;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer.;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC010327; AAH10327.1; -.  
 DR PIR; S68213; S68213.  
 DR HSSP; P01783; IIGC.  
 DR MGD; MGI:2144967; AU044919.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 71.8%; Score 516.5; DB 2; Length 473;  
 Best Local Similarity 72.5%; Pred. No. 4.5e-43;  
 Matches 100; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

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Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKKPGASLKLSCAASGFTFSNYGMSSWVRQNS   60  
        |: |::|::||::||||:::||:||:||||| || | ||||| ::|| |  
Db      1 MDSRLNLVFLVLILKGVCQLVESGGGLVKKPGRSRLSCAASGFTFSDYGMHWVRQAP    60  
  
Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNLTLYLQMSSLKSEDTALYYCVRYDH  120  
       :| |:::: | ||         ||:| |||||::|::|::|::|::|::|:| | |:  
Db     61 EGGLEWVAYINSGSTTIYYADTVKGRFTISRDNAKNTLFLOMTSLRSEDAMYYCAR-EL  119  
  
Qy    121 YSGSSDYWGQGTTVTIVSS 138  
       :          |||||::|||  
Db    120 WLRRIDYWGOGTITIVSS 137
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## HV54 MOUSE

```

AC      P18525;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V region 5-84 precursor.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/cJ;
RX      MEDLINE=89279149; PubMed=2499654;
RA      Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT      "Early onset of somatic mutation in immunoglobulin VH genes during the
RT      primary immune response.";
RL      J. Exp. Med. 169:2007-2019(1989).
CC      -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
DR      PIR; JT0505; HVMS84.
DR      HSSP; P01810; 2FBJ.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL          1          19
FT      CHAIN           20        117      Ig heavy chain V region 5-84.
FT      DOMAIN          20        49      Framework-1.
FT      DOMAIN          50        54      Complementarity-determining-1.
FT      DOMAIN          55        68      Framework-2.
FT      DOMAIN          69        85      Complementarity-determining-2.
FT      DOMAIN          86        117     Framework-3.
FT      DISULFID        41        115     By similarity.
FT      NON_TER         117        117
SQ      SEQUENCE      117 AA; 12872 MW; 234055CB6A469861 CRC64;

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Best Local Similarity 84.6%; Pred. No. 2.6e-43;

Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 ||||| ||||| |||||:||||| ||||| |||||  
 Db 1 MNFGLSLIFLVLVLKGVLCCEVKLVESGGGLVQPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117  
 :||||| | :||| ||| | |||||:|||| | ||||| |||||:|||| |  
 Db 61 EKRLEWVAYISNGGGSTYYPDTVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAR 117

# RESULT 8

HV55\_MOUSE

ID HV55\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18526;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 345 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/cJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
 primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.  
 DR PIR; JT0502; HVMS34.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 Ig heavy chain V region 345.  
 FT DOMAIN 20 49 Framework-1.  
 FT DOMAIN 50 54 Complementarity-determining-1.  
 FT DOMAIN 55 68 Framework-2.  
 FT DOMAIN 69 85 Complementarity-determining-2.  
 FT DOMAIN 86 117 Framework-3.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 70.9%; Score 510; DB 1; Length 117;  
 Best Local Similarity 83.8%; Pred. No. 4.1e-43;  
 Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 ||||| ||||| |||||:||||| ||||| ||||| ||||| |||||  
 Db 1 MNFGLRLIFLVLTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISR ENAKNTLYLQMSLKS EDTALYYCVR 117  
 :||||||| | |||| ||| | |||||||||:|||||||||:|||||  
 Db 61 EKRLEWVAYISSGGGSTYYPD TVKGRFTISR DNAKNTLYLQMSLKS EDTAMYCAR 117

RESULT 9

Q91XE1

ID Q91XE1 PRELIMINARY; PRT; 480 AA.  
 AC Q91XE1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Igh-VJ558 protein (Fragment).  
 GN Name=Igh-VJ558;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC010798; AAH10798.1; -.  
 DR HSSP; P01789; 1MCP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
FT NON\_TER 1 1  
SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match 70.2%; Score 505; DB 2; Length 480;  
Best Local Similarity 72.3%; Pred. No. 6.5e-42;  
Matches 99; Conservative 16; Mismatches 20; Indels 2; Gaps 1;

Qy 2 NFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSD 61  
| | | | | : | | | | | : | | | | | | | | | | | | | | | :  
Db 1 NFGLSLIFLVLILKGVLCVKLVESGGGLVKPGGSLRLSCAASGFIFSNYSYMSWVRQTPE 60  
  
Qy 62 KRLEWVASIRSGGGRTYYSDNVKGRETISRANAKNTLYLQMSSLKSEDTALYYCVRYDHY 121  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 61 KRLEWVATISNSGYATHYPDSMKGRETISRDNAQNTVLLQMTSLNSEDATAVYYCTRGDYW 120  
  
Qy 122 SGSSDYWGQGT TTVTVSS 138  
| | | | |  
Db 121 --YFDVWGAGT TTVTVSS 135

# RESULT 10

Q96BB9

ID Q96BB9 PRELIMINARY; PRT; 597 AA.  
AC Q96BB9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";



RL Cell 24:625-637(1981).

RN [2]

RP SEQUENCE OF 17-136.

RX MEDLINE=77100368; PubMed=401950;

RA Adetugbo K., Milstein C., Secher D.S.;

RT "Molecular analysis of spontaneous somatic mutants.";

RL Nature 265:299-304(1977).

CC

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; J00522; AAD15290.1; -.

DR PIR; E90809; G1MS21.

DR PDB; 1IGC; X-ray; H=-.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW 3D-structure; Direct protein sequencing; Immunoglobulin V region;

KW Signal.

FT NON\_TER 1 1

FT SIGNAL <1 16

FT CHAIN 17 136 Ig heavy chain V region MOPC 21.

FT DOMAIN 115 119 D segment.

FT DOMAIN 120 136 JH4 SEGMENT.

FT DISULFID 38 112

FT CONFLICT 75 78 HYAD -> DYAH (in Ref. 2).

FT CONFLICT 89 90 DN -> ND (in Ref. 2).

FT CONFLICT 115 115 W -> H (in Ref. 2).

FT CONFLICT 120 120 Y -> W (in Ref. 2).

FT STRAND 19 23

FT STRAND 26 28

FT TURN 30 31

FT STRAND 34 41

FT HELIX 45 47

FT STRAND 50 55

FT STRAND 61 67

FT TURN 69 70

FT STRAND 74 76

FT HELIX 78 80

FT STRAND 81 81

FT TURN 82 83

FT STRAND 84 89

FT TURN 90 93

FT STRAND 94 99

FT HELIX 104 106

FT STRAND 108 114

FT TURN 118 119

FT STRAND 125 126

FT STRAND 130 134

FT NON\_TER 136 136

SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

|      |  |
|------|--|
| Qy   | 5 LSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRL 64<br> ::   :     : :     :         : :      :  |
| Db   | 2 LNLVFLVLILKGVQCVDQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWRQAPEKGL 61   |
| <br> |  |
| Qy   | 65 EWVASIRSGGGRTYYSDNVKGRFTISRNAKNTLYLQMSSLKSEDTALYYCVRYDHYS-G 123<br>         : :       :     : : : : :   : : |
| Db   | 62 EWWAYISSGSSTLHYADTVKGRFTISRDNPKNLTLFLQMTSLRSEDAMYYCARWGNYPY 121   |
| <br> |  |
| Qy   | 124 SSDYWGQGT'TVT'VSS 138<br>:      :  |
| Db   | 122 AMDYWGQGT'SVT'VSS 136  |

## RESULT 12

```

ID      HV59_MOUSE          STANDARD;          PRT;    117 AA.
AC      P18530;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V region 7-39 precursor.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/cJ;
RX      MEDLINE=89279149; PubMed=2499654;
RA      Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT      "Early onset of somatic mutation in immunoglobulin VH genes during the
RT      primary immune response.";
RL      J. Exp. Med. 169:2007-2019(1989).
CC      -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
DR      PIR; JT0507; HVMS39.
DR      HSSP; P18529; 1I8K.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL          1          19
FT      CHAIN           20          117          Ig heavy chain V region 7-39.
FT      DOMAIN          20          49          Framework-1.
FT      DOMAIN          50          54          Complementarity-determining-1.
FT      DOMAIN          55          68          Framework-2.
FT      DOMAIN          69          85          Complementarity-determining-2.
FT      DOMAIN          86          117          Framework-3.
FT      DISULFID        41          115          By similarity.
FT      NON TER         117          117

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SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

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Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      |||:||||| |||| ||| ||||| ||||| |||
Db      1 MNFGLSLIFLVLILKGVQCEVKWVESGGGSVKPGGSLKLSCAASGFTFSNYGMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVR 117
      :||||| | |||:|||||:||||:| ||||| |
Db     61 EKRLEWVASISGGVSYTYPPDSVKGRFTISRDNAKNNLYLQMNSLTSEDTALYYCAR 117

```

Q6PI81

AC Q6PI81;

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Hypothetical protein.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX NCBI TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=22388257; PubMed=12477932;

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";

RN [2]

RC TISSUE=Primary B-Cells;

RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR Pfam; PF00047; ig; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 69.4%; Score 499; DB 2; Length 478;  
 Best Local Similarity 65.5%; Pred. No. 2.6e-41;  
 Matches 97; Conservative 18; Mismatches 23; Indels 10; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 | ||| :||| :|:|||||:|||||||:| ||:|||||||:| |||||  
 Db 1 MELGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSYWMSWVRQAP 60  
  
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117  
 | ||||:|: | || |:|||||||:||||:||||:|:|:||||:| |  
 Db 61 GKGLEWVANIKQDGESEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFE 120  
  
 Qy 118 -----YDHYSGSSDYWGQGTTVTVSS 138  
 |:| | ||:|||||||  
 Db 121 STMTTVNADYYFYMDVWGKGTTTVTVSS 148

#### RESULT 14

AAH41037

ID AAH41037 PRELIMINARY; PRT; 478 AA.  
 AC AAH41037;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC041037; AAH41037.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 69.4%; Score 499; DB 2; Length 478;  
 Best Local Similarity 65.5%; Pred. No. 2.6e-41;  
 Matches 97; Conservative 18; Mismatches 23; Indels 10; Gaps 1;

QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
 | ||| :||| :|:|||||:|||||||:| ||:|||||||:| |||||  
 Db 1 MELGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSYWSWVRQAP 60  
 QY 61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117  
 | |||||:| | | |:|||||||:||||:||||:| | | |  
 Db 61 KGKLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFE 120  
 QY 118 -----YDHYSGSSDYWGQGT TVTVSS 138  
 | :| | ||:|||||  
 Db 121 STMTTVNADYFFYMDVWGKGT TVTVSS 148

# RESULT 15

Q6GMV2

ID Q6GMV2 PRELIMINARY; PRT; 606 AA.  
 AC Q6GMV2;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC073758; AAH73758.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 4.  
 DR Pfam; PF00047; ig; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 4.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114E4C55 CRC64;

Query Match 68.9%; Score 495.5; DB 2; Length 606;  
 Best Local Similarity 63.6%; Pred. No. 7.6e-41;  
 Matches 98; Conservative 18; Mismatches 21; Indels 17; Gaps 2;

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | |||| :||| ::|||||:|:||||||| ||:|||||||:| |||:|
Db      1 MEFGLSWVFLVAIIKGVQCQVQLVESGGGLVKPGGSLRLSCAASGFTFSYYMSWIRQAP 60

Qy     61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
      | ||||: | | | |:|:|||||||:||||:||||:|::| |||:| |
Db     61 GKGLEWVSYISSSSSYTNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGN 120

Qy    118 -----YDHYSGSSDYWGQGT TVTVSS 138
      | :| | | |||||
Db    121 GIAAAGRVVYAEDYIIYYG-MDVWGQGT TVTVSS 153
  
```

Search completed: December 13, 2004, 19:17:46  
 Job time : 133.356 secs